

	Query Match	100.0%	Score 2308;	DB 9;	Length 2309;
	Best Local Similarity	100.0%	Pred NC 0,		
	Matches 2309; Conservative	0;	Mismatches	0;	Gaps
QY	1 AGAGGGGAGAGGAAAAACACAGACAAGACTCTCAGGCTTCCCTGTGAGGCATGCAACCCCCCAC	60			
Dd	1 AGAGGGGAGAGGAAAAACAGACAAAGACTCTCAGGCTTCCCTGTGAGGCATGCAACCCCCCAC	60			

QY 61 CTCTCCAGGGATCTCATTAAGAGTGTTTAGCTGGGAGGTGTAAAGCCAGGCGCTGGGA 120  
DB 61 CTCTCCAGGGATCTCATTAAGAGTGTTTAGCTGGGAGGTGTAAAGCCAGGCGCTGGGA 120  
QY 121 GACAGGGCAGAGTGTCTAGAGTGTCTCTCAACCCCTTCAGTGGGCTAGCTGGT 180  
DB 121 GACAGGGCAGAGTGTCTAGAGTGTCTCTCAACCCCTTCAGTGGGCTAGCTGGT 180  
QY 181 GTGTGTCTAAGAGCCCAAGAGCAAGAGTCTACAGAGAGGCCCAAGAGCCCTCT 240  
DB 181 GTGTGTCTAAGAGCCCAAGAGCAAGAGTCTACAGAGAGGCCCAAGAGCCCTCT 240  
QY 241 CAGACAGTCAAGGCACTAGTGTCCCACTTCAGAGTCTCTCAAGGCAAGAGGTGTGA 300  
DB 241 CAGACAGTCAAGGCACTAGTGTCCCACTTCAGAGTCTCTCAAGGCAAGAGGTGTGA 300  
QY 301 CATCTCAACCCCAAGAGCAAGAGTCTACAGAGAGGCCCAAGAGGTGTGA 360  
DB 301 CATCTCAACCCCAAGAGCAAGAGTCTACAGAGAGGCCCAAGAGGTGTGA 360  
QY 361 CAGAGTCAAGTCCCAAGAGCCCAAGAGCCCAAGAGTCTCTCAAGGCAAGAGGTGTGA 420  
DB 361 CAGAGTCAAGTCCCAAGAGCCCAAGAGCCCAAGAGTCTCTCAAGGCAAGAGGTGTGA 420  
QY 421 CTGGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480  
DB 421 CTGGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480  
QY 481 TCATCTCTGTGTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
DB 481 TCATCTCTGTGTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
QY 541 TGAGTGTGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 600  
DB 541 TGAGTGTGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 600  
QY 601 CAGAGTCTTGAACAGAGGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
DB 601 CAGAGTCTTGAACAGAGGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
QY 661 TTGGAGCTGAGTCT 720  
DB 661 TTGGAGCTGAGTCT 720  
QY 721 TGCGGCTGGGCGCCGACACACCCCAAGGCTGAAACCGCTTTCTCGGCGCCGCGC 780  
DB 721 TGCGGCTGGGCGCCGACACACCCCAAGGCTGAAACCGCTTTCTCGGCGCCGCGC 780  
QY 781 TCTTGAAGGCTTGAACGAGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 840  
DB 781 TCTTGAAGGCTTGAACGAGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 840  
QY 841 CCAAGCTGATGCTTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
DB 841 CCAAGCTGATGCTTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
QY 901 TATCCGAGTACTGGGCTTGGGCGTGAAGCAAGAGTGTGTGTGTGTGTGTGTGTGT 960  
DB 901 TATCCGAGTACTGGGCTTGGGCGTGAAGCAAGAGTGTGTGTGTGTGTGTGTGTGT 960  
QY 961 GCTTTGAGGCTGTGGGCGCAAGTACTTATAGCTTTTATCTTCAAGCTGTATCTTA 1020  
DB 961 GCTTTGAGGCTGTGGGCGCAAGTACTTATAGCTTTTATCTTCAAGCTGTATCTTA 1020  
QY 1021 CTAACAGTGGGCAATACAGCGCGCGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 1080  
DB 1021 CTAACAGTGGGCAATACAGCGCGCGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 1080  
QY 1081 ACTTCTGTGGGCGCTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140  
DB 1081 ACTTCTGTGGGCGCTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140

QY 1141 ACAACATGAACACTGAGTGGGCTTTCTACCCAGATCATGCACTGTGTGAAGATGA 1200  
DB 1141 ACAACATGAACACTGAGTGGGCTTTCTACCCAGATCATGCACTGTGTGAAGATGA 1200  
QY 1201 TGAAGCTGAGCAAGTCAACCGAGCTGAGAGGCGAGTTATTGACTGTGTATCAGACC 1260  
DB 1201 TGAAGCTGAGCAAGTCAACCGAGCTGAGAGGCGAGTTATTGACTGTGTATCAGACC 1260  
QY 1261 TGAAGTCAACCAAGAGTGAACCAAGAGTGAAGTCAAGAGTCAAGAGTCAAGAGTCA 1320  
DB 1261 TGAAGTCAACCAAGAGTGAACCAAGAGTGAAGTCAAGAGTCAAGAGTCAAGAGTCA 1320  
QY 1321 TGGGCGAGAGT 1380  
DB 1321 TGGGCGAGAGT 1380  
QY 1381 AGAATGTGAGGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
DB 1381 AGAATGTGAGGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
QY 1441 CACAGGTTGAATATGTATGCGCAAGAGCAATTTGCGCAAGAGTGTATCATTCGAG 1500  
DB 1441 CACAGGTTGAATATGTATGCGCAAGAGCAATTTGCGCAAGAGTGTATCATTCGAG 1500  
QY 1501 AGGTTCAACTGCGCGT 1560  
DB 1501 AGGTTCAACTGCGCGT 1560  
QY 1561 GGTCTACTTTGGGAGATGAGCATTCATCAATCAAGAGGAAAGTGTGTGTGTGTGTGT 1620  
DB 1561 GGTCTACTTTGGGAGATGAGCATTCATCAATCAAGAGGAAAGTGTGTGTGTGTGTGT 1620  
QY 1621 GCACAGCAATCAATCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
DB 1621 GCACAGCAATCAATCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
QY 1681 TGGGAGAGT 1740  
DB 1681 TGGGAGAGT 1740  
QY 1741 AGATCTGT 1800  
DB 1741 AGATCTGT 1800  
QY 1801 AGAGGCGCAGAGTCCGCGCTACAGAGCTTACAGAGCTGTGTGTGTGTGTGTGTGTGT 1860  
DB 1801 AGAGGCGCAGAGTCCGCGCTACAGAGCTTACAGAGCTGTGTGTGTGTGTGTGTGTGT 1860  
QY 1861 AGTTGT 1920  
DB 1861 AGTTGT 1920  
QY 1921 AACGCTGT 1980  
DB 1921 AACGCTGT 1980  
QY 1981 ACAGAGTGAAGCTGT 2040  
DB 1981 ACAGAGTGAAGCTGT 2040  
QY 2041 GACCCCGAGTCAAGAGTCAACCCCAATCCCAATCCCAAGATTTCCACTCTGTATGAAT 2100  
DB 2041 GACCCCGAGTCAAGAGTCAACCCCAATCCCAATCCCAAGATTTCCACTCTGTATGAAT 2100  
QY 2101 CAGAGTTGATGAAGCTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160  
DB 2101 CAGAGTTGATGAAGCTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160  
QY 2161 ACAGAGCAATTTGT 2220  
DB 2161 ACAGAGCAATTTGT 2220  
QY 2221 GCCCCCACTTACAGTACACACACACACACACACACACACACACACACACACACCTGT 2280



QY 1021 CTACAGTGGGCGATACACCGCGCCGACGAGGGAAGAGTACTCTTCATGTGTGGCG 1080  
DB 1467 CTACAGTGGGCGATACACCGCGCCGACGAGGGAAGAGTACTCTTCATGTGTGGCG 1526  
QY 1081 ACTTCTCTGCGCGGCTCATGGGTTTGGCCACCATCATGGGTAGCATGAGCTGTGATCT 1140  
DB 1527 ACTTCTCTGCGCGGCTCATGGGTTTGGCCACCATCATGGGTAGCATGAGCTGTGATCT 1586  
QY 1141 ACAACATGAACACTGACAGATGCGGCTTTCTACCCAGATCATGCACTGGTGAAGAAGTACA 1200  
DB 1587 ACAACATGAACACTGACAGATGCGGCTTTCTACCCAGATCATGCACTGGTGAAGAAGTACA 1646  
QY 1201 TGAAGCTGCACACGTCAACCGCAGAGTGGAGCGGCGCATTTTGAATGGTATCAGACCC 1260  
DB 1647 TGAAGCTGCACACGTCAACCGCAGAGTGGAGCGGCGCATTTTGAATGGTATCAGACCC 1706  
QY 1261 TGCAGATCAACAGAAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGC 1320  
DB 1707 TGCAGATCAACAGAAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGC 1766  
QY 1321 TGCAGGCGAAGAGT 1380  
DB 1767 TGCAGGCGAAGAGT 1826  
QY 1381 AGAAGCTGTGAGGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
DB 1827 AGAAGCTGTGAGGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1886  
QY 1441 CACAGAGTGAATATGTATGCGCGAAGAGAGACATTTGGCCAGAGATGTACATCCGAG 1500  
DB 1887 CACAGAGTGAATATGTATGCGCGAAGAGAGACATTTGGCCAGAGATGTACATCCGAG 1946  
QY 1501 AGGCTCAACTGCGCGT 1560  
DB 1947 AGGCTCAACTGCGCGT 2006  
QY 1561 GGGCTTACTTTGGGAGATGACGATCATCAATCAAGGGAACAATGTCTGGGAACCGCC 1620  
DB 2007 GGGCTTACTTTGGGAGATGACGATCATCAATCAAGGGAACAATGTCTGGGAACCGCC 2066  
QY 1621 GCACAGCCCAACATCAAGAGCCTAGGTTATTCAGACCTTATTCGCTGAGCAAGAGACC 1680  
DB 2067 GCACAGCCCAACATCAAGAGCCTAGGTTATTCAGACCTTATTCGCTGAGCAAGAGACC 2126  
QY 1681 TGCAGGAGT 1740  
DB 2127 TGCAGGAGT 2186  
QY 1741 AGATCTCTGTGAATAATGAACAAGTTGACGTGATGAGGCGACGTGAGTCGCCCTGC 1800  
DB 2187 AGATCTCTGTGAATAATGAACAAGTTGACGTGATGAGGCGACGTGAGTCGCCCTGC 2246  
QY 1801 AGAGAGCCACAGAGTCCGCGCTACAGAGGCTTACAGCAGCAGCTGATGATCTACAGACA 1860  
DB 2247 AGAGAGCCACAGAGTCCGCGCTACAGAGGCTTACAGCAGCAGCTGATGATCTACAGACA 2306  
QY 1861 AGTTTGTCTGCTCTCTGT 1920  
DB 2307 AGTTTGTCTGCTCTCTGT 2366  
QY 1921 AACGGTGTGAGTGTGAGATCTGAGAGTGGCCAAATGCGAGGACCTGGCTGAGAGCTGAT 1980  
DB 2367 AACGGTGTGAGTGTGAGATCTGAGAGTGGCCAAATGCGAGGACCTGGCTGAGAGCTGAT 2426  
QY 1981 ACGAGGGGTAGCTGTGAGAGGGAATCTTCAAAAGATGAAGAGGAGGAGGCGCAGAGAG 2040  
DB 2427 ACGAGGGGTAGCTGTGAGAGGGAATCTTCAAAAGATGAAGAGGAGGAGGCGCAGAGAG 2486  
QY 2041 GACCCCCAGGTCCAGAGTACCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCAT 2100  
DB 2487 GACCCCCAGGTCCAGAGTACCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCAT 2546  
QY 2101 CAGAG 2105

DB 2547 CAGAG 2551

RESULT 3  
US-10-174-333-29  
; Sequence 29, Application US/10174333  
; Publication No. US20040029220A1  
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APPLICANT: Padigaru, Muralidhara  
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APPLICANT: Burgess, Catherine E.  
APPLICANT: Gangolli, Beba A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Rastelli, Luca  
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APPLICANT: Grose, William M.  
APPLICANT: Szekeres, Edward S.  
APPLICANT: Alsobrook, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Li, Li  
APPLICANT: Zhong, Mei  
TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-783 CIP1  
CURRENT FILING DATE: 2002-06-18  
PRIOR APPLICATION NUMBER: US/10/174,333  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 60/193,664  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/194,614  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/195,063  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,066  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,067  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,068  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,069  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,070  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,510  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/219,855  
PRIOR FILING DATE: 2000-07-21  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: CuroseqList version 0.1  
SEQ ID NO: 29  
LENGTH: 2551  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (779) ..(2503)  
US-10-174-333-29

Query Match 91.1%; Score 2101.8; DB 13; Length 2551;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2103; Conservative 0; Mismatches 0; Gaps 0;



QY	1	AAGGGGAGAGAGAAAAACAGACAAAGCTAGGCTTCCTCTGAGGATGACCCAC	60
Db	447	AGAGGGAGAGAGAAAAACAGACAAAGCTAGGCTTCCTCTGAGGATGACCCAC	507
QY	61	CTTCTCCAGGGATCTCATTTAGAGGGTTTACTGGGCGAGGTAAAGCCAGGCTTGGG	120
Db	507	CTTCTCCAGGGATCTCATTTAGAGGGTTTACTGGGCGAGGTAAAGCCAGGCTTGGG	566
QY	121	GACAGGGCAGAGTGTAGAGCTAGACTGTCTCAACCCCTTAGTAGAGGCTAGCTTG	187
Db	567	GACAGGGCAGAGTGTAGAGCTAGACTGTCTCAACCCCTTAGTAGAGGCTAGCTTG	626
QY	181	GTGTGTCTAAGAGCCCCCAAGACAAAGAGTACAGACAGAAAGCCCAAGAGGCTCTT	240
Db	627	GTGTGTCTAAGAGCCCCCAAGACAAAGAGTACAGACAGAAAGCCCAAGAGGCTCTT	686
QY	241	CAGACAGTCAGGCACTAGTGGCCCAATCCAAATCCCCCTTACAGGCAAGAGGTTGGA	300
Db	687	CAGGCAAGTCAGGCACTAGTGGCCCAATCCAAATCCCCCTTACAGGCAAGAGGTTGGA	746
QY	301	CATCTCACACCCAGCACAAGACCACAGAAACATGAGCCAGGACCCAAAGTAAAGCA	360
Db	747	CATCTCACACCCAGCACAAGACCACAGAAACATGAGCCAGGACCCAAAGTAAAGCA	806
QY	361	CAGAGTCAATGTCCTCCGAGCCCATCCAGGCCCAGAAAGTTGCTGCTGTCTTGAACCAT	420
Db	807	CAGAGTCAATGTCCTCCGAGCCCATCCAGGCCCAGAAAGTTGCTGCTGTCTTGAACCAT	866
QY	421	CTGGGGATTTCTACTACTGTGTGGCTGAACATAGTGTCTTCCAGTCAATGTATACCTCA	480
Db	867	CTGGGGATTTCTACTACTGTGTGGCTGAACATAGTGTCTTCCAGTCAATGTATACCTCA	926
QY	481	TCACTCTGTGTGACAGAGCTGTCCCGACTTGCAGACAGGTTATCTGTGGGCTGGT	540
Db	927	TCACTCTGTGTGACAGAGCTGTCCCGACTTGCAGACAGGTTATCTGTGGGCTGGT	986
QY	541	TGGTGTGTGACATACAGAGTACCTGTCTATACCTATAGACATGTGTGAGCTTCCACA	600
Db	987	TGGTGTGTGACATACAGAGTACCTGTCTATACCTATAGACATGTGTGAGCTTCCACA	1044
QY	601	CAGGATTTCTTGGAACAGGGGATCTGTGTGTGAGCAAGGTAGATCTTGAGTGGCTACG	660
Db	1047	CAGGATTTCTTGGAACAGGGGATCTGTGTGTGAGCAAGGTAGATCTTGAGTGGCTACG	1106
QY	661	TTGCGACTGTGAAGTTCTTCTTGAACTGGCTTCCCTGATGCCACAGATGTGATCTACG	720
Db	1107	TTGCGACTGTGAAGTTCTTCTTGAACTGGCTTCCCTGATGCCACAGATGTGATCTACG	1166
QY	721	TGCGGTGGGGCCCGACACCCACCTGAGGCTGAACCGCTTCTTCCGCGCGCCCGCC	780
Db	1167	TGCGGTGGGGCCCGACACCCACCTGAGGCTGAACCGCTTCTTCCGCGCGCCCGCC	1226
QY	781	TCCTTGAAGGCTTTCGACCGCACAGAGACCCCGACAGCTTACCCAAATGCTTTGGCATG	840
Db	1227	TCCTTGAAGGCTTTCGACCGCGAGAGACCCCGACAGCTTACCCAAATGCTTTGGCATG	1286
QY	841	CCAAGCTATGCTTTACATTTTGTGTATCCATTGGACAGCTGCTATACTTTGGCC	900
Db	1287	CCAAGCTATGCTTTACATTTTGTGTATCCATTGGACAGCTGCTATACTTTGGCC	1346
QY	901	TATCCCGGTACTGGGGCTTGGGGGTGACGATGGGTATACCGGACCCCGCGACGCTG	960
Db	1347	TATCCCGGTACTGGGGCTTGGGGGTGACGATGGGTATACCGGACCCCGCGACGCTG	1406
QY	961	GCTTTGAGCGGCTGTGGGCGACAGTACCTCTATAGCTTTTACTTTCACAGGTATCTGA	1020
Db	1407	GCTTTGAGCGGCTGTGGGCGACAGTACCTCTATAGCTTTTACTTTCACAGGTATCTGA	1466
QY	1021	CTACAGTGGGATACACCGCGCCGACAGGAGAAAGATACCTTTGATGTGGGCG	1080
Db	1467	CTACAGTGGGATACACCGCGCCGACAGGAGAAAGATACCTTTGATGTGGGCG	1526
QY	1081	ACTTCTGCTGGGCGGTATGGGTTTGGCCACATCATGGGTAGATAGCTCTGTATCTT	1140

Db	1527	ACTTCTGCTGGCCGTCATGGTTTGGCCACCAATCATGGGTAGATAGGCTCTCTCATCT	1586
QY	1141	ADPACTGAACA CTGCGAGATGGCGCTTTTACCCAGATCATGCACTGTGAGAAATACA	1200
Db	1587	ACAACTGAACA CTGCGAGATGGCGCTTTTACCCAGATCATGCACTGTGAGAAATACA	1646
QY	1201	TGAAGCTGAGACGTCGAACCGCAAGCTGAGACGGCGATTATTGACTGTATCGACAC	1260
Db	1647	TGAAGCTGAGACGTCGAACCGCAAGCTGAGACGGCGATTATTGACTGTATCGACAC	1706
QY	1261	TGCAATCAACAAGAAAGATGACCAAGAGATGGCATCTTACAGCACTTGGCTGAGGGC	1320
Db	1707	TGCAATCAACAAGAAAGATGACCAAGAGATGGCATCTTACAGCACTTGGCTGAGGGC	1766
QY	1321	TGCGGCGAAGAGTGGCTGTGTCTGTGCACTGTGCACTGTGACCGCGGTGCGATCTTTC	1380
Db	1767	TGCGGCGAAGAGTGGCTGTGTCTGTGCACTGTGCACTGTGACCGCGGTGCGATCTTTC	1826
QY	1381	AGAACTGAGAGCCAGCTGCTGCGAAGAGAGTGGTCTGAAGCTGACGCCCCAGACCTACT	1440
Db	1827	AGAACTGAGAGCCAGCTGCTGCGAAGAGAGTGGTCTGAAGCTGACGCCCCAGACCTACT	1886
QY	1441	CACCAAGTGAATATATATATGCGCAAGAGGACATTTGGCCAAAGATGTACTATCTCCAG	1500
Db	1887	CACCAAGTGAATATATATATGCGCAAGAGGACATTTGGCCAAAGATGTACTATCTCCAG	1946
QY	1501	AGGGTCAACTGGCCGTGGTGGCAGATGTATGATCACAAGTATGGTGTGCTCGGTCCAG	1560
Db	1947	AGGGTCAACTGGCCGTGGTGGCAGATGTATGATCACAAGTATGGTGTGCTCGGTCCAG	2006
QY	1561	GGCTCTACTTTGGGGAGATCGACATCATCAATCAAGGAAACATGTCTGGGAAACCGCC	1620
Db	2007	GGCTCTACTTTGGGGAGATCGACATCATCAATCAAGGAAACATGTCTGGGAAACCGCC	2066
QY	1621	GCAAGGCAACATCAAGAGCTTAGTATTTAGACCTTATCTGCTGAGCAAGAGGACCC	1680
Db	2067	GCAAGGCAACATCAAGAGCTTAGTATTTAGACCTTATCTGCTGAGCAAGAGGACCC	2126
QY	1681	TGCGGAGGTGTCTGAGGAGTATCCAGACGACACCATCATGAGGAGAAAGGACGCTG	1740
Db	2127	TGCGGAGGTGTCTGAGGAGTATCCAGACGACACCATCATGAGGAGAAAGGACGCTG	2186
QY	1741	AGATCCCTGCGAAATATTAACAAGTTGACGTGAATCTGAGGCAAGTATGCGCTTGC	1800
Db	2187	AGATCCCTGCGAAATATTAACAAGTTGACGTGAATCTGAGGCAAGTATGCGCTTGC	2246
QY	1801	AGAGGCAACAGAGTCCCGGCTACGAGGCTAGACCGAGAGCTGGATTAATTACAGACCA	1860
Db	2247	AGAGGCAACAGAGTCCCGGCTACGAGGCTAGACCGAGAGCTGGATTAATTACAGACCA	2306
QY	1861	AGTTTGTGCTCTCTGAGCTGAGTGTCCAGGCACTTAAATTGCTTACCGCATTTG	1920
Db	2307	AGTTTGTGCTCTCTGAGCTGAGTGTCCAGGCACTTAAATTGCTTACCGCATTTG	2366
QY	1921	AAAGGCTGAGTGGCAGATCTCGAGAGTGTGCAATGCTCCGAGAGCTGTGAGGCTGATG	1980
Db	2367	AAAGGCTGAGTGGCAGATCTCGAGAGTGTGCAATGCTCCGAGAGCTGTGAGGCTGATG	2426
QY	1981	ACGAGGTTAGCTTGGAGAGGAACTTCCAAATGAAAGAGGAGGAGGCGACGCCAGAGG	2040
Db	2427	ACGAGGTTAGCTTGGAGAGGAACTTCCAAATGAAAGAGGAGGAGGCGACGCCAGAGG	2486
QY	2041	GACCCCAAGTCCAAGTGAACCCCATCCCATCCAGAGATTCGACCTCTAGTGAATC	2100
Db	2487	GACCCCAAGTCCAAGTGAACCCCATCCCATCCAGAGATTCGACCTCTAGTGAATC	2546
QY	2101	CAGAG 2105	
Db	2547	CAGAG 2551	

## RESULT 4





QY 1542 TATGCTGCTCGTGCAGAGGCTCTACTTTGGGAGATCAGCATCATCAATCAAGG 1601  
Db 1848 TATGCTGCTCGTGCAGAGGCTCTACTTTGGGAGATCAGCATCATCAAGG 1907  
QY 1602 AACATGCTGGAAACCGCCGCAAGCCAAATCAAGAGCTTGTATTCAGACCTATTC 1661  
Db 1908 AACATGCTGGAAACCGCCGCAAGCCAAATCAAGAGCTTGTATTCAGACCTATTC 1967  
QY 1662 TCCCTGAGAGAGAGAGCTGCGGAGGTGTGAGAGTATTCAGAGAGAGAGCATC 1721  
Db 1968 TCCCTGAGAGAGAGAGCTGCGGAGGTGTGAGAGTATTCAGAGAGAGAGCATC 2027  
QY 1722 ATGAGAGAGAGAGAGAGAGTCTGCTGAAATGAAAGTGTGAGAGAGAGAGAG 1781  
Db 2028 ATGAGAGAGAGAGAGAGAGTCTGCTGAAATGAAAGTGTGAGAGAGAGAGAG 2087  
QY 1782 GCAGCTGAGATCGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1841  
Db 2088 GCAGCTGAGATCGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2147  
QY 1842 CTGAGATGATCTAG 1901  
Db 2148 CTGAGATGATCTAG 2207  
QY 1902 AGATGCTTACCGCATTTGAAACCGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1961  
Db 2208 AGATGCTTACCGCATTTGAAACCGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2267  
QY 1962 GACCTGCTGAG 2021  
Db 2268 GACCTGCTGAG 2327  
QY 2022 GCGAGGCGCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2060  
Db 2328 GCGAGGCGCAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2366

## RESULT 6

US-09-842-758-27

Sequence 27, Application US/09842758

Publication No. US20030083244A1

GENERAL INFORMATION:

APPLICANT: Vernet, Corine A. M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Gerlach, Valerie

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APPLICANT: Malyankar, Uriel M.

APPLICANT: Boldog, Ferenc L.

APPLICANT: Zernusen, Bryan D.

APPLICANT: Spylek, Kimberly A.

APPLICANT: Majumder, Kumud

APPLICANT: Tchernev, Velizar T.

APPLICANT: Padigara, Muralidhara

APPLICANT: Patuturajan, Meera

APPLICANT: Burgess, Catherine E.

APPLICANT: Gangoli, Bsha A.

APPLICANT: Smithson, Glenda

APPLICANT: Rastelli, Luca

APPLICANT: MacDougall, John R.

APPLICANT: Taupier, Raymond J.

APPLICANT: Grose, William M.

APPLICANT: Edward, Szekeles S.

APPLICANT: Alsobrook II, John P.

TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-783

CURRENT APPLICATION NUMBER: US/09/842,758

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/200,158

PRIOR FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: 60/200,613

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,780

PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/201,006  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,007  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,236  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,238  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/201,186  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,474  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/201,508  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 60/220,591  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/232,678  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/263,217  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/265,160  
PRIOR FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 1835  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-842-758-27

Query Match 77.4%; Score 1785.4; DB 10; Length 1835;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1825; Conservative 0; Mismatches 1; Indels 9; Gaps 3;

QY 280 TACAGGAG 339  
Db 1 TACAGGAG 60  
QY 340 AGGACACCAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 396  
Db 61 AGGACACCAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 120  
QY 397 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456  
Db 121 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 457 TCTTCCAGTATGATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACTG 516  
Db 181 TCTTCCAGTATGATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACTG 240  
QY 517 AGCAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576  
Db 241 AGCAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 577 TAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 633  
Db 301 TAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
QY 634 ACAAGGTAAGATCTCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 693  
Db 361 ACAAGGTAAGATCTCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 694 CCTGATGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 753  
Db 421 CCTGATGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
QY 754 TGAACCGCTTTCTCG 813  
Db 481 TGAACCGCTTTCTCG 540  
QY 814 CAGCTTACCAATGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873



ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (54) .. (1787)  
US-10-174-333-27

Query Match 77.4%; Score 1785.4; DB 13; Length 1835;  
Best Local Similarity 99.5%; Pired. No. 0;  
Matches 1825; Conservative 0; Mismatches 1; Indels 9; Gaps 3;

QY 280 TAAAGGACAGAGAGGCTGTGACATCTCACACCCAGACAGACCAAGACATGAGCC 339  
DB 1 TACAGGACAGAGAGGCTGTGACATCTCACACCCAGACAGACCAAGACATGAGCC 60  
QY 340 AGGACACCAAGAGAGAGACACACAGAGTCCAGTCCCGCCAGCCCATCCAGAGCC--AGGA 396  
DB 61 AGGACACCAAGAGAGAGAGACACACAGAGTCCAGTCCCGCCAGCCCATCCAGAGAGGA 120  
QY 397 AGTTGCTGCTGTCTGTGACATCTGAGGATTAATCTACTGTGTGCTGAACAAATGG 456  
DB 121 AGTTGCTGCTGTCTGTGACATCTGAGGATTAATCTACTGTGTGCTGAACAAATGG 180  
QY 457 TCTTCCAGACATGATTAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 516  
DB 181 TCTTCCAGACATGATTAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240  
QY 517 AGCAGGCTTATCTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576  
DB 241 AGCAGGCTTATCTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300  
QY 577 TAGACATGT 633  
DB 301 TAGACATGT 360  
QY 634 ACAAGGAGAGATCTGAGT 693  
DB 361 ACAAGGAGAGATCTGAGT 420  
QY 694 CCTGTATCCCAAGATGT 753  
DB 421 CCTGTATCCCAAGATGT 480  
QY 754 TGAACCGCTTCTCG 813  
DB 481 TGAACCGCTTCTCG 540  
QY 814 CAGCTTACCCAAATGCTGT 873  
DB 541 CAGCTTACCCAAATGCTGT 600  
QY 874 ATTGAGACAGTCTCTATATCTTGTGCTTATCCCGGTACTGTGTGTGTGTGTGTGTGTGT 933  
DB 601 ATTGAGACAGTCTCTATATCTTGTGCTTATCCCGGTACTGTGTGTGTGTGTGTGTGTGT 660  
QY 934 GGGTGTATCCCGGACCCCG 993  
DB 661 GGGTGTATCCCGGACCCCG 720  
QY 994 GCTTTTACTTCTCCAGCGTATGATCTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053  
DB 721 GCTTTTACTTCTCCAGCGTATGATCTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
QY 1054 AAGAGAGATGCTCTTCAATGT 1113  
DB 781 AAGAGAGATGCTCTTCAATGT 840  
QY 1114 TATGT 1173  
DB 841 TATGT 900  
QY 1174 CAGATATGACATGT 1233  
DB 901 CAGATATGACATGT 960

QY 1234 GGCGAGTTATGATGTGTATGACACCTGACATCAACAGAGATGACCAAGAGCTGAG 1293  
DB 961 GGCGAGTTATGATGTGTATGACACCTGACATCAACAGAGATGACCAAGAGAGCTGAG 1020  
QY 1294 CCATCTTACAGACCTTGTGCTGTGAGCGGCTGCGGACAGAGTGTGTGTGTGTGTGTGTGT 1353  
DB 1021 CCATCTTACAGACCTTGTGCTGTGAGCGGCTGCGGACAGAGTGTGTGTGTGTGTGTGTGT 1080  
QY 1354 CCATCTTACAGCGGCTGTGAGATCTTTCAGAACCTGTGAGGCGACCTGTGTGTGTGTGTGT 1413  
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QY 1414 TGCTGAAGCTGACCGCCAGACCTTACTCAACAGATGATATGTATGTGTGTGTGTGTGTGT 1473  
DB 1141 TGCTGAAGCTGACCGCCAGACCTTACTCAACAGATGATATGTATGTGTGTGTGTGTGT 1200  
QY 1474 TTGGCCAGAGATGTATCATATCTCCAGAGAGGTCACTGTGCGGTGTGTGTGTGTGTGT 1533  
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DB 1261 TCACACATGTATGT 1320  
QY 1594 TCACACATGTATGT 1650  
DB 1321 TCACACATGTATGT 1380  
QY 1651 CAGACCTATTTCTGCTGTGAGCAAGAGAGACCTGTGCGGAGGTGTGTGTGTGTGTGTGT 1710  
DB 1381 CAGACCTATTTCTGCTGTGAGCAAGAGAGACCTGTGCGGAGGTGTGTGTGTGTGTGTGT 1440  
QY 1711 CACAGACCATATGAG 1770  
DB 1441 CACAGACCATATGAG 1500  
QY 1771 TGAATGTGTGAGGAGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1830  
DB 1501 TGAATGTGTGAGGAGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560  
QY 1831 TAGACACAGCTGT 1890  
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QY 1891 CAGAGGCACTTAAGATGT 1950  
DB 1621 CAGAGGCACTTAAGATGT 1680  
QY 1951 CAATGCCGAGAGACCTGTGCTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2010  
DB 1681 CAATGCCGAGAGACCTGTGCTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
QY 2011 AAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2070  
DB 1741 AAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
QY 2071 ATCCCGAGATTCACACCTCTAGTGAATCCAGAG 2105  
DB 1801 ATCCCGAGATTCACACCTCTAGTGAATCCAGAG 1835

RESULT 8  
US-09-735-932-1  
Sequence 1, Application US/09735932  
Patent No. US20020037548A1  
GENERAL INFORMATION:  
APPLICANT: GUEGLER, Karl et al  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000663  
CURRENT APPLICATION NUMBER: US/09/735, 932





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? PRIOR APPLICATION NUMBER: 09/7735,932
? PRIOR FILING DATE: 2000-12-14
? PRIOR APPLICATION NUMBER: 60/211,223
? PRIOR FILING DATE: 2000-06-13
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1758
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)...(1758)
? OTHER INFORMATION: n = A,T,C or G
? GS-10-207-951-1

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Query Match	75.5%	Score 1742.6	DB 15	Length 1758
Best Local Similarity	99.8%	Prod. No. 0		
Matches 1745	Conservative	0	Mismatches	4
			Indels	0
			Gaps	0
QY	325	ACAGAACCATGAGCCAGGACACCCAAAGTGAGACAAACAGATGTCAGATCCCCACGCCCAT	384	
Db	3	ACAGAACCATGAGCCAGGACACCCAAAGTGAGACAAACAGATGTCAGATCCCCACGCCCAT	62	
QY	385	CCAAAGGCCAGAAAGTTCCTGCTGCTGCTGAGACCATCTGGGAGTTTCTACTAGTGGAGC	444	
Db	63	CCAAAGGCCAGAAAGTTCCTGCTGCTGCTGAGACCATCTGGGAGTTTCTACTAGTGGAGC	122	
QY	445	TGAACACAAATGATCTTCCAGTCAATGTATTAACCTCATCATCTCTGTGTGAGAGCTGCT	504	
Db	123	TGAACACAAATGATCTTCCAGTCAATGTATTAACCTCATCATCTCTGTGTGAGAGCTGCT	182	
QY	505	TCCCCGACTTGACAGACGGTTATCTGGTGGCTGGTGGTGGTGGAGCTACACAGAGTACC	564	
Db	183	TCCCCGACTTGACAGACGGTTATCTGGTGGCTGGTGGTGGTGGAGCTACACAGAGTACC	242	
QY	565	TGCTATACCTACTATGACATGGTGGTGGCTTCCACACAGAAATCTTTGGAAACAGGGATCC	624	
Db	243	TGCTATACCTACTATGACATGGTGGTGGCTTCCACACAGAAATCTTTGGAAACAGGGATCC	302	
QY	625	TGTGTGTGACAAAGGATAGATCTTCAGATGCTACGTTTGGCACCTGGAGATTTCTTTGG	684	
Db	303	TGTGTGTGACAAAGGATAGATCTTCAGATGCTACGTTTGGCACCTGGAGATTTCTTTGG	362	
QY	685	ACCTGGCTTCCCTGATGCGCCACACATGAGTGCATACGTGCGGCTGGGCGCACACACCA	744	
Db	363	ACCTGGCTTCCCTGATGCGCCACACATGAGTGCATACGTGCGGCTGGGCGCACACACCA	422	
QY	745	CCCTGAGGCTGAACCGGCTTTCGCGCGCGCCCGCTTTGAGAGCTTTGACCGGCACAG	804	
Db	423	CCCTGAGGCTGAACCGGCTTTCGCGCGCGCCCGCTTTGAGAGCTTTGACCGGCACAG	482	
QY	805	AAGCCCGCACAGCTTAACCCAAATGCTTGGATGCGCAAGCTGATGCTTATACATTTTGG	864	
Db	483	AAGCCCGCACAGCTTAACCCAAATGCTTGGATGCGCAAGCTGATGCTTATACATTTTGG	542	
QY	865	TGCTCATTCATTGGAACAGAGTGCCTATATCTTGGCCCTATCCCGGTAAGCTGGAGCTTGGAGC	924	
Db	543	TGCTCATTCATTGGAACAGAGTGCCTATATCTTGGCCCTATCCCGGTAAGCTGGAGCTTGGAGC	602	
QY	925	GTGACGCATGGGTGTATCCCGGACCCCGCGGACCGTGGCTTGAAGGCGCTGGGCGGCAGT	984	
Db	603	GTGACGCATGGGTGTATCCCGGACCCCGCGGACCGTGGCTTGAAGGCGCTGGGCGGCAGT	662	
QY	985	ACCTCATATAGCTTTTACTTCTCCAGCGGTATCTGATCAAGTGGGCGATACACCGCGCG	1044	
Db	663	ACCTCATATAGCTTTTACTTCTCCAGCGGTATCTGATCAAGTGGGCGATACACCGCGCG	722	
QY	1045	CAGCCAGGAGAAAGAGTACTCTTCTATGGTGGGCACTTCTGTGGCCGTCATAGGGTT	1104	
Db	723	CAGCCAGGAGAAAGAGTACTCTTCTATGGTGGGCACTTCTGTGGCCGTCATAGGGTT	782	
QY	1105	TGCGCACATCATGGGTAGCATAGGCTGTATCTATCAACATGAAACCTGCAGATGGCG	1164	

Db	783	TCGCACCACTCATGGGTACGATGAGCTGTGTCATCTTACAACTGAACACTGCAGATGGGG	842
QY	1165	CTTTCTACCCGAGTCAATGCATCTGGTGAAGAAATCAATGAAGCTGAGACGTCACCGCA	1224
Db	843	CTTTCTACCCGAGTCAATGCATCTGGTGAAGAAATCAATGAAGCTGAGACGTCACCGCA	902
QY	1225	AGCTGAGCGGCGAGTTATTTGACTGGTATCAACACTGCAGATCAACAAGATGACCA	1284
Db	903	AGCTGAGCGGCGAGTTATTTGACTGGTATCAACACTGCAGATCAACAAGATGTC	962
QY	1285	ACGAGTAGGCATCTTAAACAACACTTGGCTGAGCGCTGCGGCAAGAAATGCTGTGCTG	1344
Db	963	ACGAGTAGGCATCTTAAACAACACTTGGCTGAGCGCTGCGGCGAGAAAGTGTGTCTG	1022
QY	1345	TGCACCTGTGTCATCTGAGCCGGGTGCAATCTTTTCAAGACTGTGAGGCGACCTGTG	1404
Db	1023	TGCACCTGTGTCATCTGAGCCGGGTGCAATCTTTTCAAGACTGTGAGGCGACCTGTG	1082
QY	1405	AGGAGCTGGTCTGAGCTGACGCCAGACCTACTCACCAGGTGAATATGATGCGCGA	1464
Db	1083	AGGAGCTGGTCTGAGCTGACGCCAGACCTACTCACCAGGTGAATATGATGCGCGA	1142
QY	1465	AAGGAGCATTTGGCCAAAGAAATGTACATCTCGAAGGGTCAACTGGGCGCTGTGGCGAG	1524
Db	1143	AAGGAGCATTTGGCCAAAGAAATGTACATCTCGAAGGGTCAACTGGGCGCTGTGGCGAG	1202
QY	1525	ATGATGTGTTATCAACAGTATCTGTGTGCTGGGTGAGGGCTCTACTTTGGGGAGATGAGA	1584
Db	1203	ATGATGTGTTATCAACAGTATCTGTGTGCTGGGTGAGGGCTCTACTTTGGGGAGATGAGA	1262
QY	1585	TCATCAATCAAAAGGGAACATGTCTGGGAAACCGCGCACAGCCCAATCAAGAGCTT	1644
Db	1263	TCATCAATCAAAAGGGAACATGTCTGGGAAACCGCGCACCAACATCAAGAGCTT	1322
QY	1645	GTTATTCAGACTTATTTGCTCTGACCAAGAGAGACTTGCGGGAGGTGCTGAGGAGATC	1704
Db	1323	GTTATTCAGACTTATTTGCTCTGACCAAGAGAGACTTGCGGGAGGTGCTGAGGAGATC	1382
QY	1705	CACAGACCAAGCATCAATGAGGAGAAAGAGACGTAGATCTTGCTGAAAAATGAACAAT	1764
Db	1383	CACAGACCAAGCATCAATGAGGAGAAAGAGACGTAGATCTTGCTGAAAAATGAACAAT	1442
QY	1765	TGGAAGCTGATCTGAGGCAAGCTGAGATGCGCTTCGAGAGGCCACAGAGTCCCGGTAC	1824
Db	1443	TGGAAGCTGATCTGAGGCAAGCTGAGATGCGCTTCGAGAGGCCACAGAGTCCCGGTAC	1502
QY	1825	GAGGCTTGAACACAGAGCTGTGATATCTACAGACCAATTTGCTCGCTCTGCTGAGC	1884
Db	1503	GAGGCTTGAACACAGAGCTGTGATATCTACAGACCAATTTGCTCGCTCTGCTGAGC	1562
QY	1885	TGGAGTCCAGCGCACTTAAATTTGCTTACCCGATTTGAACGAGCTGAGAGTGCAGACTCGAG	1944
Db	1563	TGGAGTCCAGCGCACTTAAATTTGCTTACCCGATTTGAACGAGCTGAGAGTGCAGACTCGAG	1622
QY	1945	AGTGGCCAAATGCCCCGAGAGCTTGGCTGAGGCTGTGATCGAGGGTGAAGCTTGAAGAGGAA	2004
Db	1623	AGTGGCCAAATGCCCCGAGAGCTTGGCTGAGGCTGTGATCGAGGGTGAAGCTTGAAGAGGAA	1682
QY	2005	CTTTCAAAGATTGAAGGGGCAAGGCCAGACAGAGGGAAACCCCAAGTCCAGAGTACCCC	2064
Db	1683	CTTTCAAAGATTGAAGGGGCAAGGCCAGACAGAGGGAAACCCCAAGTCCAGAGTACCCC	1742
QY	2065	ATCCCCATC 2073	
Db	1743	ATCCCCATC 1751	

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RESULT 10
US-09-927-267-3
; Sequence 3, Application US/09927267
; Publication No. US20020182691A1
; GENERAL INFORMATION:

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QY	1750	TGAAAATGAAACAAGTTGGACGTGAATGCTGAGGAGACGTGAGATGCGCCTTCAGAGAGCCA	1809
Db	61	TGAAAATGAAACAAGTTGGACGTGAATGCTGAGGAGACGTGAGATGCGCCTTCAGAGAGCCA	120
QY	1810	CAGAGTCCCGGCTACAGAGCCTAGACACAGACAGCTGATGATCTACAGACCAAGTTTGCTC	1869
Db	121	CAGAGTCCCGGCTACAGAGCCTAGACACAGACAGCTGATGATCTACAGACCAAGTTTGCTC	180
QY	1870	GCTCTCTGACTAGCTGAGTGCACGCGCATTTAAGATTGCTTACCAGATTGAAGGCTGG	1929
Db	181	GCTCTCTGACTAGCTGAGTGCACGCGCATTTAAGATTGCTTACCAGATTGAAGGCTGG	240
QY	1930	AGTGGCAGACTGAGAGAGTGGCCAAAGCCCGAGGACCTGAGCTGATGACAGAGGTG	1989
Db	241	AGTGGCAGACTGAGAGAGTGGCCAAAGCCCGAGGACCTGAGCTGATGACAGAGGTG	300
QY	1990	AGCTGAGGAGGGGAATTCCAAAGATGAAGAGGGGACGAGGCCAGGAGGAGACCCCGAG	2049
Db	301	AGCTGAGGAGGGGAATTCCAAAGATGAAGAGGGGACGAGGCCAGGAGGAGACCCCGAG	360
QY	2050	GTCAGAGTACCCCATCTCCCATCTCCAGAGATTCCCACTCTCTAATGAATCAAGATTGT	2109
Db	361	GTCAGAGTACCCCATCTCCCATCTCCAGAGATTCCCACTCTCTAATGAATCAAGATTGT	420
QY	2110	AGTAAAGCTTAATCTGCTGCAACTCTCTCACTCTGCTGAGATCAACAGACACAGAGCG	2169
Db	421	AGTAAAGCTTAATCTGCTGCAACTCTCTCACTCTGCTGAGATCAACAGACACAGAGCG	480
QY	2170	AATTGCTGTAGATGCCAGCTAGAGATATAGAGATTAAAGCAATTCAAGCCCCACT	2229
Db	481	AATTGCTGTAGATGCCAGCTAGAGATATAGAGATTAAAGCAATTCAAGCCCCACT	540

QY AGGAAGTTGCTGCTGTCTCTGAGCCATTCTGGGATTACTACTGTTGGGTGAACA 452  
 |||||  
 Db AAGAGGATGCGATCGGTGGAGCCGTCGAGCAACTGTACTACCGCTGGCTGACGCC 522  
 |||||  
 QY ATGCTCTTCCAGTCATGTAATACTTCATCTCTGTGGAGGCCGCTTCCCGAC 512  
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 Db ATGCCCTGCGCTGCTCTTAATACTGGTATCTGCTTATTGACAGGCCGCTTTGCATGG 582  
 |||||  
 QY TTGCAGACAGGTTATCTGTGGCGCTGTGTGTGCTGGAATAACAGAGTACCTGCTATAC 572  
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 Db CTGCAAGCCAGATACCTGATGCTGTGGCTGTGCTGTGACTACTCGGACAGATGCTCTGTA 642  
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 QY CTACTAGCATGTGTGTGGCGCTTCCACACAGGATTTCTGGAACAGGCGCATCCGTGATGG 632  
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 Db GTCTTGATGTGCTTGTACGAGCTCGACAGGTTTCTCGACGACAGGCTTAATGTCAGT 702  
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QY 633 GACAAAGGATGATCTCGAGTCGATCGTTCGACCTGAGATTTCTTTGGACCTGGCT 692  
Db 703 GATACCAAGAGGCTGTGGCAGCATTTACAAGACGACGACGATTCAGCTGATGTGTG 762  
QY 693 TCCCTGATGCCCAACAGATGTGTCTACGTGGGCTGGGCGGCAACACCCAGCTGAG 752  
Db 763 TCCCTGTGTCCCAACGACCTGGCTTACTTAAGATGTGGCAAACTACCCAGAAAGTGA 822  
QY 753 CTGAACCGCTTTCTCCGCGCGCGCGCTTTTGAAGGCTTTCAGAGCTTTCAGAGACAG 812  
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QY 813 ACAGCTTACCCAAATGCGCTTTCGCAATGCGCAAGCTGATCTTTCATTTTGTGTGATC 872  
Db 883 ACCAATACCCCAATATGTTCAAGATGTGGAACTTGTCTTGTACTTCACTTCACTATC 942  
QY 873 CATTGGAACAGTGTCTTACTTTTCCCTATCCCGGTACCTGGGCTTGGGCGGTGACCA 932  
Db 943 CACTGGAATGCTGTGATCTTACTTTCCTTCCAACTTCACTTGTGGGACAGACTCC 1002  
QY 933 TGGGTGTACCCGGAACCCCGGACCTGGCTTTGAGCGCTTGGCGGCGCACTACCTCTAT 992  
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QY 993 AGCTTTACTTCTCCAGCTGATATCTGATCACTAGTGGCGATACACCGCGCGCAGCAGG 1052  
Db 1063 AGTCTCTACTGTGTCACTTGAACCTTACCAACCAATGTGTGAGACCCCAACCCCGTAAA 1122  
QY 1053 GAAGAAGATACCTCTTCACTGTGTGGGCACTTCTGCTGGCGCTCATGGGTTTGGCACC 1112  
Db 1123 GATGAGAGATATCTTTGTGTGTGATCTTCTTGGTGTGTGATTTTGTGATTTTGGCACC 1182  
QY 1113 ATCATGGGTGATGATGATCTGTGATCTAACAATGAACTGCGAGATGGCGCTTTCTAC 1172  
Db 1183 ATGTGTGGCAATGTGGGCTCCATGATCTCGAATATGATGCTTCAAGGCGAGATTCAG 1242  
QY 1173 CCAGATCATGCACTGGGAGAGATGATATGATGATGATGATGATGATGATGATGATG 1232  
Db 1243 GCCAAGTATATTCATCAAGCAGTATGATGATGATGATGATGATGATGATGATGATG 1302  
QY 1233 CGGCGAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1292  
Db 1303 AGCGGGTATATCGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1362  
QY 1293 GCCATCTTACAGCATCTTGGCTGAGCGGCTTGGCGGCAAGTGTGTGTGTGTGTGTG 1352  
Db 1363 GAGGTGTCTCAAGGCTTCCAGCAAGCTGAGGCTGAGATGCTCAACGTGACCTG 1422  
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QY 1413 GTGCTGAAGCTGCAAGCCCGACCTTACTCAGGAGTGAATATGTATGCGGCAAGGAGC 1472  
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Db 1603 GTCAACCCAGT 1662  
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QY 1653 GACCTATCTGT 1712  
Db 1723 GACCTATCTGT 1782

QY 1713 CAGACCATGAGAGAGAAAGGAGCTGATCTTCTGTGAATAATGACAAGTTGAGCTG 1772  
Db 1783 AAGAGGCTCTGAGAGAGAAAGGAGCGGAGATCTGTGATGAAA---GACAACTGATGAT 1839  
QY 1773 AATGTGAAGGAGCTGAGATGCTTCCAGAGAGGCGACAGAGATCCCGGCTACGAGGCT 1832  
Db 1840 GAGGAGCTGGCCAGGCGGCGGCGGAGCCCAAGAGACTTGAAGAGAAAGTGAAGCAGCTG 1899  
QY 1833 GACCAAGCAGCTGATGATCTACAGACCAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1892  
Db 1900 GGGTCTCTGTGACACCTGTGAGACAGGTTTGCACCGCTCTGTGTGTGTGTGTGTGTGT 1959  
QY 1893 AGCGACTTAAGATGCTTACCGCATTTGAAGGCTGTGAGCTGAG 1937  
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Job time : 1081.8 secs





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 11, 2004, 01:41:30 ; Search time 749 Seconds

(without alignments)  
3862.651 Million cell updates/sec

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 3304383 seqs, 2515761380 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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11: /cgn2\_6/ptodata/2/pubna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubna/US09\_NEW\_PUB.seq:\*  
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15: /cgn2\_6/ptodata/2/pubna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubna/US10\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/2/pubna/US10\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query \*  
No. Score Match Length DB ID Description

1	2989	100.0	1728	6	US-09-927-267-3	Sequence 3, Appli
2	2989	100.0	1728	9	US-10-189-507-2	Sequence 2, Appli
3	2989	100.0	2308	9	US-09-927-267-2	Sequence 2, Appli
4	2989	100.0	2308	9	US-10-302-172-351	Sequence 351, App
5	2984	99.8	2013	17	US-10-311-624-2	Sequence 2, Appli
6	2984	99.8	2551	10	US-09-842-758-29	Sequence 29, Appli
7	2984	99.8	2551	13	US-10-174-333-29	Sequence 29, Appli
8	2976	99.6	1755	9	US-09-735-932-1	Sequence 1, Appli
9	2976	99.6	1758	15	US-10-207-951-1	Sequence 1, Appli
10	2957.5	98.9	1835	10	US-09-842-758-27	Sequence 27, Appli
11	2957.5	98.9	1835	13	US-10-174-333-27	Sequence 27, Appli
12	2266	75.8	10989	15	US-09-735-923-3	Sequence 3, Appli
13	2266	75.8	10989	15	US-10-207-951-3	Sequence 3, Appli
14	1565	52.4	3027	15	US-10-295-573-1	Sequence 1, Appli
15	1558	52.1	1995	15	US-10-087-217-1	Sequence 1, Appli
16	1558	52.1	3027	15	US-10-295-573-4	Sequence 4, Appli
17	1554	52.0	1995	15	US-10-087-217-5	Sequence 5, Appli
18	1554	52.0	3027	15	US-10-295-573-2	Sequence 2, Appli
19	1549.5	51.8	2085	15	US-10-345-680-27	Sequence 27, Appli
20	1549.5	51.8	3486	15	US-10-345-680-25	Sequence 25, Appli
21	1549	51.8	1995	15	US-10-087-217-3	Sequence 3, Appli
22	1545	51.7	1995	15	US-10-087-217-7	Sequence 7, Appli
23	1535	51.4	1995	9	US-09-735-927-1	Sequence 1, Appli
24	1535	51.4	1995	14	US-10-034-843-1	Sequence 1, Appli
25	1535	51.4	1995	15	US-10-168-651-34	Sequence 34, Appli
26	1535	51.4	1995	16	US-10-189-507-1	Sequence 1, Appli
27	1535	51.4	2111	15	US-10-114-193-17	Sequence 17, Appli
28	1532	51.3	2190	15	US-10-029-677-23	Sequence 23, Appli
29	1531	51.2	1995	16	US-10-189-507-4	Sequence 4, Appli
30	1529	51.2	2186	15	US-10-029-677-1	Sequence 1, Appli
31	1526.5	51.1	2500	13	US-10-342-887-427	Sequence 427, App
32	1526.5	51.1	2500	13	US-10-172-118-427	Sequence 427, App
33	1494	50.0	2877	15	US-10-295-573-3	Sequence 3, Appli
34	1341.5	44.9	12017	9	US-09-735-927-3	Sequence 3, Appli
35	716	24.0	2607	16	US-10-189-507-3	Sequence 3, Appli
36	716	24.0	4382	16	US-10-159-653-147	Sequence 147, App
37	655	21.9	2430	12	US-09-855-828-3	Sequence 3, Appli
38	655	21.9	2703	12	US-09-855-828-2	Sequence 2, Appli
39	655	21.9	2757	12	US-09-855-828-16	Sequence 16, Appli
40	612	20.5	601	15	US-10-207-951-24	Sequence 24, Appli
41	467.5	15.6	4751	13	US-10-311-795-5	Sequence 5, Appli
42	467.5	15.6	5065	15	US-10-067-457-4	Sequence 4, Appli
43	467.5	15.6	5499	13	US-10-276-774-973	Sequence 973, App
44	465.5	15.6	3372	15	US-10-067-457-2	Sequence 2, Appli
45	465.5	15.6	3459	13	US-10-311-795-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-927-267-3  
Sequence 3, Application US/09927267  
Publication No. US20020182691A1  
GENERAL INFORMATION:  
APPLICANT: Crech, Christopher D.  
APPLICANT: Jegla, Timothy J.  
TITLE OF INVENTION: Channel  
FILE REFERENCE: 018512-006510US  
CURRENT APPLICATION NUMBER: US/09/927, 267  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/226, 253  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1728  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)

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; OTHER INFORMATION: coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(1728)
; OTHER INFORMATION: CNG2B
US-09-927-267-3

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Alignment Scores:	
Pred. No.:	0
Score:	2989.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Gaps:	0
Length:	1728
Matches:	575
Conservative:	0
Mismatches:	0
Indels:	0

US-09-927-267-1 (1-575) x US-09-927-267-3 (1-1728)

QY		MeSerGIaApThrLyValIysThrGluSerSerProAlaProSerIysAla	20
Db	1	ATGAGCCAGGACACCAAGTAGAACACACAGTCCAGTCCCCAGCCCATCCAAAGCC	60
QY		ArgIysLeuLeuProValIleuAspProSerGIaAspIYrYrYrYrTriPLeuAsnThr	40
Db	61	AGGAAGTTGTCGCTGCTGGAGCCCATCTGGGGATTTACTACTCGGGGCTGAACAA	120
QY		MetValPheProValMetTyrAsnIleIleLeuValCysArgAlaCysPheProAsp	60
Db	121	ATGGCTTTCCAGATGATGATTAACCTCATACCTCGTGGTGAAGACCTGCTTCCCCAG	180
QY		LeuGlnHisGIYrYrLeuValAlaTriPLeuValIleuAspIYrYrThrSerAspLeuLeuYr	80
Db	181	TTGCAGCAGCAGGTTACTCGGTGGCCGTGGTTGGTGGTGAACTAACAGAGTACCTGCTATAC	240
QY		LeuLeuAspMetValAlaArgPheHisThrArgIYPheLeuGluGlnGlyIleLeuValVal	100
Db	241	CTACTAGACATGTGTGGTGGCTTCACACAGGATTTCTGGAACAGGGCATCTGTGGTGGT	300
QY		AspIysGIaArgIISerSerArgIYrYrValAcGlnTriPSerPhePheLeuAspLeuAla	120
Db	301	GACAAAGGTAGATCTCGAGTGCCTACGTTCCGACCTGGAGTTCTTCTTGGACCTGGCT	360
QY		SerLeuMetProThrAspValValIYrYrValArgLeuGlyProHisThrProThrLeuArg	140
Db	361	TCCCTGATGCCACAGATGTGTCTACAGTGGCGCTGGGGCCGACACACCCACCCGAGG	420
QY		LeuAsnArgPheLeuArgIaProArgLeuPheGlnAlaPheAspArgThrGlnThrArg	160
Db	421	CTGAACCGGCTTCTCCGGCGCGCCGCTTCTTGAGGCTTGACCGCGCACAGAGACCCG	480
QY		ThrAlaIYrProAsnAlaPheArgIleAlaIYsLeuMetLeuYrIlePheValValIle	180
Db	481	ACAGCTTACCCAAATGCCCTTTGCGATTGCGACAGCTGATGCTTAACTTTTGGCTGCATC	540
QY		HisTriPAsnSerCysLeuYrPheAlaLeuSerArgTyrLeuGlyPheGlyArgAspAla	200
Db	541	CATTGGAAACGCTGCTTACTTATCTTGCCCATACCCGCTACTCGGCTTCGGGCTGACGCA	600
QY		TriPValTyrProAspProAlaGlnProGlyIYPheGluArgPheuArgArgIYrIYrLeuYr	220
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QY		SerPheTyrPheSerThrIleuIleuThrThrValGIaSpThrProProProAlaArg	240
Db	661	AGCTTTTACTTCTCCACGCGTACATGACTACAGTGGCGCATACACCGCGCGACGACG	720
QY		GluGluGluTyrIleuPheMetValGIaAspPheLeuLeuAlaIleMetGIYPheAlaThr	260
Db	721	GAGAAAGACTCTTTCATGGGGGAGCTTCTGTGGCCGTATGGGTTCGCCACC	780
QY		IleMetGIYSerMetSerSerValIleIYrAsnMetAsnThrAlaAspAlaIaPheYr	280
Db	781	ATCATGTGGTGAACATGAGCTCTGTCATCTAACATGAACATGACATGCGGCTTTTAC	840
QY		ProAspHisAlaLeuValIYsIYrMetIYsLeuGlnHisValAsnArgIYsLeuGlu	300

Db	CCAGATCAAGCACTGGTGAAGAATGACATGAAGCTGCAGACGTCAACCGCAAGCTGGAG	900
QY	ArgArgValIleAspTrpTrglnHisLeuGlnIleAsnIleYsMetThrAsnGluVal	320
Db	CGCGCAGTATTGACTGCTGATACAGCACTGCAGATATCAACAAGATGACCAACGAGGTA	960
QY	AlaIleLeuGlnHisLeuProGluArgLeuAspAlaGluValAlaValSerValHisLeu	340
Db	GCCATTTACAGCACTTGCTTACGCGCGCTGCGGCGCAAGATGGCTGTCTGTGCACCTG	1020
QY	SerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGlnLeu	360
Db	TTCACCTGAGCGCGGTGCAGATCTTTCAGAACGTGAGGCCAGCTGCTGAGAGACTG	1080
QY	ValLeuIysLeuGlnProGlnThrTrpSerProGlnValuTrpValYsArgIysGlyAsp	380
Db	GTGCTGAAGTGGAGGCCCAAGACCTTCAACCAAGGTAATATGATATGCCCAAGAGAC	1140
QY	IleGlyGlnGluMetTrpIleIleArgGlnGlnLeuAlaValAlaAspAspGly	400
Db	ATTGGCCAAAGATGTATCATCTCCAGAGGGCTCACTGGCCCTGTGTGGAGATGATGCT	1200
QY	IleThrGlnTrpAlaValLeuGlnYalArgIleuTrpPheGlyGlnIleSerIleIleAsn	420
Db	ATCACACAGTATGCTGTGCTCGGTGCAGGGCTCTACTTGGGAGAGATCAGCATCATCAAC	1260
QY	IleYsGlyAsnMetSerGlyAsnAlaArgTrpAlaAsnIleYsSerLeuGlyTrpSer	440
Db	ATCAAAAGGAAACATGTCTGGAAACCGCCGCAAGCCAAATCAAGACCTTAAGTTATCA	1320
QY	AspLeuPheCysLeuSerIysGluAspLeuArgGluValLeuSerGluTrpProGlnAla	460
Db	GACCTATTCTGCTTGACCAAGAGGACTTCGGGAGGTGCTGACCAAGTATCCACAAGCA	1380
QY	GlnThrIleMetGlnGluIysGlyArgGluIleLeuLeuIysMetAsnIysLeuAspVal	480
Db	CAGGCATCATGAGAGGAAAGGACGTGAGATCCTGCTGAAAATGAACAAGTTGAGAGTG	1440
QY	AsnAlaGluAlaAlaGluIleAlaLeuGlnGluAlaThrGluSerArgLeuArgGlyLeu	500
Db	AATGCTAGGCAAGTGTAGATGCGCTGCAGAGGCCACAAGATCCCGGCTACAGAGGCTTA	1500
QY	AspGlnGlnIleuAspAspLeuGlnThrLysPheAlaArgLeuLeuAlaGluLeuGlnSer	520
Db	GACCAGACGCTGATGATCTACACACCAAGTTGCTGCTCTCGGCTGAGAGCTGAGATCC	1560
QY	SerAlaLeuIysIleAlaTrpArgIleGluArgLeuGlnTrpGlnThrArgIuTrpPro	540
Db	AGCGCACTTAAGATGTCTTACCGCATTTGAACCGGTGAGTGCGACATCCGAGATGGCCA	1620
QY	MetProGluAspLeuAlaGluAlaAspAspGlnGlyGluProGlnGlnGluTrpSerLys	560
Db	ATGCCCAAGAGACCTCGGCTGAGGCTGATGACAGAGGCTAGCTGAGAGAGGAATTTCCAA	1680
QY	AspGlnGlnGlyArgAlaSerGlnGlnGlyProProGlyProGln	575
Db	GATAAAGAGGCGCAGGCCACGCCAGAGGAGACCCCAAGTCCAGAG	1725
RESULT 2		
US-10-189-507-2		
; Sequence 2, Application US/10189507		
; Publication No. US20030228633A1		
; GENERAL INFORMATION:		
; APPLICANT: ZOLLER, MARK		
; APPLICANT: XU, HONG		
; APPLICANT: STASZEWSKI, LENA		
; APPLICANT: MOYER, BRYAN		
; APPLICANT: PRONIN, ALEX		
; APPLICANT: ADLER, JON ELLIOT		
; APPLICANT: SERVANT, GUY		
; APPLICANT: CALLAMARRA, NICHOLAS		
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC		







Db 2079 AATCTGAGGAGCTGAGATGCGCTTGGAGAGGCCACAGAGTCCCGGCTACAGAGCTTA 2138  
 QY 501 AspgIngluLeuAspAspLeuGlnThrIysPheAlaArgLeuLeuAlaGluLeuGluSer 520  
 Db 2139 GACACGAGCGTGGATGATCTACAGACCAGATTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2198  
 QY 521 SerAlaLeuIysIleAlaIleTyrArgIleGluArgLeuGluIlePheGlnThrPro 540  
 Db 2199 AGCGCACTTAAGATTGCTTACCGCATTTGACCGCTGGAGTGGCGACTCGAGAGTGGCCA 2258  
 QY 541 MetProGluAspLeuAlaGluAlaAspAspGluGluProGluGluGluIleThrSerIys 560  
 Db 2259 ATGCCCGAGGACCTGGCTGAGGCTGATGACGAGGCTGAGCTGAGAGGAACTTCCAAA 2318  
 QY 561 AspgIngluIleArgAlaSerGlnGluIleProProGluIleProGlu 575  
 Db 2319 GATGAAAGGAGGAGGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2363

## RESULT 5

US-10-311-624-2  
 ; Sequence 2, Application US/10311624  
 ; Publication No. US20040127683A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.  
 ; APPLICANT: RAUMANN, Brigitte E.  
 ; APPLICANT: Sanjamwala, Madhu S.  
 ; APPLICANT: TRIBOULEY, Catherine M.  
 ; APPLICANT: Walla, Nalinder K.  
 ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS  
 ; FILE REFERENCE: SI-0141 PCT  
 ; CURRENT APPLICATION NUMBER: US/10/311,624  
 ; PRIOR FILING DATE: 2002-12-17  
 ; PRIOR APPLICATION NUMBER: 60/215,391  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 2  
 ; LENGTH: 2013  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 6703242CBI  
 ; US-10-311-624-2

Alignment Scores:  
 Pred. No.: 0 Length: 2013  
 Score: 2984.00 Matches: 574  
 Percent Similarity: 99.83% Conservative: 0  
 Best Local Similarity: 99.83% Mismatches: 1  
 Query Match: 99.83% Indels: 0  
 DB: 17 Gaps: 0

US-09-927-267-1 (1-575) x US-10-311-624-2 (1-2013)

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 Db 124 ATGAGGCAAGACCAAGAGTGAAGACAGAGTCCAGTCCCGCAGCCCATTCAGAGGCC 183  
 QY 21 ArgIysLeuLeuProValIleuAspProSerGlyAspTyrIleTyrIleThrIleuAsnThr 40  
 Db 184 AGGAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243  
 QY 41 MetValPheProValMetIleIleLeuValCysArgAlaCysPheProAsp 60  
 Db 244 ATGGTCTTCCAGTCAATGATAACCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303  
 QY 61 LeuGlnHisGlyTyrIleuValAlaIlePheValIleuAspTyrThrSerAspLeuLeuTyr 80  
 Db 304 TTGCACACGAGTATCTGGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 363  
 QY 81 LeuLeuAspMetValValArgPheHisThrGlyPheLeuGluGlnGlyIleLeuValVal 100

Db 364 CTACTAGACATGATGATGCTGCTTCCACAGAGATTCTTGAACAGAGGACCTGATGCTG 423  
 QY 101 AspyIsgIlyArgIleSerSerArgTyrValArgThrIlePhePheLeuAspLeuAla 120  
 Db 424 GACAAAGGATAGATCTGAGTGTCTAGCTTGCACTGGAGATTCTTCTTGGACTGCTGCT 483  
 QY 121 SerLeuMetProThrAspValIleTyrValArgLeuGlyProHisThrProThrLeuArg 140  
 Db 484 TCCCTGATGCCCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543  
 QY 141 LeuAsnArgPheLeuAlaGluAlaProArgLeuPheGluAlaPheAspArgThrGlnThrArg 160  
 Db 544 CTGAACCGCTTTCCTCCGCGCGCCCGCTCTTCAGAGGCTTTCAGACCGCAGAGAGCCCGC 603  
 QY 161 ThrAlaTyrProAsnAlaPheArgIleAlaIleIysLeuMetLeuTyrIlePheValValIle 180  
 Db 604 AAGCTTACCCCAATGCTCTTCCGATTCGCACTGAGCTGATGCTTACATTTTGTCTATTC 663  
 QY 181 HisTrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrIleuGlyPheGlyArgAspAla 200  
 Db 664 CATTGAAACAGCTGCTATACCTTTCCTTATCCCGTATCCGCTGCTGCTGCTGCTGCTGCTGCT 723  
 QY 201 TrpValTyrProAspProAlaGlnProGlyPheGluArgLeuArgArgGlnThrIleuTyr 220  
 Db 724 TGGGTGTACCCGAGACCCGCGCAGCTGGCTTTGAGCCCTGGCGGCGCAGTACCTTAT 783  
 QY 221 SerPheTyrPheSerThrLeuIleuThrThrValGlyAspThrProProProAlaArg 240  
 Db 784 AGCTTTTACTTCCCGACCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 843  
 QY 241 GluGluGluTyrLeuPheMetValGlyAspPheLeuLeuAlaValMetGlyPheAlaThr 260  
 Db 844 GAGAAAGAGTACCTCTTCATGCTGGGCGACCTTCCTGCGCGCTGATGGGTTCGCCACC 903  
 QY 261 IleMetGlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaIlePheTyr 280  
 Db 904 ATCATGGGTAGCATGATGCTGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 963  
 QY 281 ProAspHisAlaLeuValIleIysTyrMetCysLeuGlnHisValAsnArgIysLeuGln 300  
 Db 964 CCGATCATGCACTGCTGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023  
 QY 301 ArgArgValIleAspTrpTyrGlnHisLeuGlnIleAsnIysIysMetThrAsnGluVal 320  
 Db 1024 CGGCGAGTATTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083  
 QY 321 AlaIleLeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSerValHisLeu 340  
 Db 1084 GCCATCTTAACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
 QY 341 SerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGluIleu 360  
 Db 1144 TCCACTCTGAGCGGGGTGCAGATCTTTCAGAACTGAGAGCCAGCTGCTGAGGAGAGCTG 1203  
 QY 361 ValLeuIysLeuGlnProGlnThrTyrSerProGlyGluTyrValCysArgIysGlyAsp 380  
 Db 1204 GTGCTGAAGCTGAGCCCGCAGACCTACTCAGAGGATATGATGATGATGATGATGATGATGAT 1263  
 QY 381 IleGlyGlnGluMetTyrIleIleArgGluGluGlnLeuAlaValAlaAspAspGly 400  
 Db 1264 ATTTGGCCAAAGATGATGATCTCCAGAGGGGTCAACTGGCTGCTGCTGCTGCTGCTGCTGCT 1323  
 QY 401 IleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGluIleSerIleIleAsn 420  
 Db 1324 ATCAGACATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1383  
 QY 421 IleIysGlyAsnMetSerGlyAsnArgGlnAlaAsnIleIysSerLeuGlyTyrSer 440  
 Db 1384 ATCAAGGGAACATGCTGGGAAACCCCGCAGCCAGCCAAATCAAGAGCCATGATTTTCA 1443  
 QY 441 AspLeuPheCysLeuSerIysGluAspLeuArgGluValIleuSerGluTyrProGlnAla 460  
 Db 1444 GACCTATTCTGCTGCTGAGCAAGAGGAGACCTGGGGAGGTGCTGAGCGAGTATCCAGAGCA 1503





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Db      1439 AGCTTTACTTCTCCAGCTGATACATGAGTGGGCTATCACCGCCGACGAGG 1498
QY      241 GUGUGUGUUTYrleuphemeValIGLYAspPheleuleuAlaValMetGlyPheAlaThr 260
Db      1499 GAGAGAGAGTACTCTTCATGAGTGGGAGTCTTCTGTCGCCGCTGAGGTTTCCGACCC 1558
QY      261 IImetGlySerMetSerSerValIleTYrAsnMetAsnThrAlaAspAlaAlaPheTYr 280
Db      1559 ATCATGGGTAGCATGACCTGCTGATCATCAACAATGAACTGCAGATGGGGCTTTTCTAC 1618
QY      281 ProAspHisAlaLeuValIlySlyTYrMetIlySleuGlnHisValIAsnArgIlySleuGlu 300
Db      1619 CCATATCATGACATGGTGAAGAAAGTACATGAAGCTGACAGCATCAACCGACCTGGAG 1678
QY      301 ArgArgValIleAspTYrGlyGlnHisIleuGlnIleAsnIlySmetThrAsnGluValI 320
Db      1679 CGGGAGATTATGACTGGTATCACCACTTGAGATCAACAAGAAAGATGACCAAGAGTA 1738
QY      321 AlaIleuGlnHisIleuProGluArgLeuArgAlaGluValAlaValSerValHisIleu 340
Db      1739 GCCATCTTACAGCACTTGCTGACGCGGCTGCGGCGACAGAGGCTGTGTCTGTCACCTG 1798
QY      341 SerThrIleuSerArgValGlnHisIleuPheGlnAsnCysGluIleAsnIleuGluIleu 360
Db      1799 TCCACTGTGAGCCCGGTGCAGATCTTTCAGAACTGTGAGGCCAGCTGCTGAGAGAGCTG 1858
QY      361 ValIleuIlySleuGlnProGlnThrTYrSerProGlyIlyTYrValCysArgIlySlyAsp 380
Db      1859 GTGCTGAAGCTGACGCCCCACACCTACTCACAGGTGAAATGATGTGCGCAAAAGGAAAC 1918
QY      381 IleGlyIleuMetTYrIleIleArgGluGlyIleuAlaValAlaAspAspGly 400
Db      1919 ATTGGCCAAAGAGTATCATCATCCGAGAGGTCAACTGCGGTGTGTGTCAGATGATGCT 1978
QY      401 IleThrGlyIlyTYrAlaValIleuGlyValIleuTYrPheGlyGluIleSerIleIleAsn 420
Db      1979 ATCAACAGTATGCTGTGCTGCTGCTGAGGCTCTTCTTGGGAGATCAGCATCATCAAC 2038
QY      421 IleIlySlyAsnMetSerGlyAsnArgArgThrAlaAsnIleIlySerIleuTYrSer 440
Db      2039 ATCAAGAGGAAACATCTCTGGGAAACCGCGCAAGCAACATCAAGCACTAGTTATTCA 2098
QY      441 AspleuPheCysLeuSerIlyGlyAspleuArgIleuValIleuSerGluTYrProGlnAla 460
Db      2099 GACCTATTCTGCTGAGCAAGAGGAGCTGCGGAGGTGCTTACGAGATTCACAAGCA 2158
QY      461 GlnThrIleMetGluGlnIlySlyGlyArgGluIleuIleuIlyMetAsnIlySleuAspVal 480
Db      2159 CAGACCATCATGAGAGGAGAAAGAGCTGAGATCTGCTGAATAATGAACAAGTTGAGACGTG 2218
QY      481 AsnAlaGluAlaAlaGluIleuIleuGlnGlnAlaThrGluSerArgLeuArgIlyLeu 500
Db      2219 AATGCTGAGGCGAGCTGAGATCCCTGCGAGAGGCCACAGAGTCCGCTACAGAGCCCTA 2278
QY      501 AspGlnGlnIleuAspAspleuGlnThrIlySlyPheAlaArgLeuIleuAlaGluIleuGluSer 520
Db      2279 GACCGAGAGCTGATCATCATCAAGACAAATTGCTGCTCTGCTGCTGAGCTGAGGTCC 2338
QY      521 SerAlaIleuIlyIleuIleuTYrArgIleuGlyArgLeuGlyIlyProGlnThrArgIlyPro 540
Db      2339 AGGCGACCTTAAGATTCTTACCCGATTGAACGGCTGAGATGGAGAGCTGAGAGGTGCCA 2398
QY      541 MetProGluAspIleuAlaGluAlaAspAspGlyGlyGluProGluGluGlyIlyThrSerIlyS 560
Db      2399 ATGCCCGAGAGACTGCTGCTGAGCTGATGACAGAGGTGAGCTGAGAGGAGAACTTCCAAA 2458
QY      561 AspGluGluGlyArgAlaSerGlnGlyIlyProProGlu 575
Db      2459 GATGAAGAGGCGGCGAGCCAGCCAGGAGGAGCCCGCGAGTCCAGAG 2503

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RESULT 7  
US-10-174-333-29

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: Sequence 29, Application US/10174333
: Publication No. US20040029220A1
: GENERAL INFORMATION:
: APPLICANT: Vermet, Corine A.M.
: APPLICANT: Fernandes, Elma R.
: APPLICANT: Gerlach, Valerie
: APPLICANT: Malyankar, Uriel M.
: APPLICANT: Boldog, Ferenc L.
: APPLICANT: Zernhusen, Bryan D.
: APPLICANT: Spytek, Kimberly A.
: APPLICANT: Majumder, Kumud
: APPLICANT: Tchiernev, Velizar T.
: APPLICANT: Padigaru, Muraidhara
: APPLICANT: Patnrajan, Meera
: APPLICANT: Burgess, Catherine E.
: APPLICANT: Gargolli, Beba A.
: APPLICANT: Smithson, Glenda
: APPLICANT: Rastelli, Luca
: APPLICANT: MacDougall, John R.
: APPLICANT: Taupier, Raymond J.
: APPLICANT: Grose, William M.
: APPLICANT: Szekeres, Edward S.
: APPLICANT: Alsobrook, John P.
: APPLICANT: Anderson, David W.
: APPLICANT: Guo, Xiaojia (Sasha)
: APPLICANT: Li, Li
: APPLICANT: Zhong, Mei
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 15966-783 CIP1
: CURRENT APPLICATION NUMBER: US/10/174,333
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: 60/193,664
: PRIOR FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: 60/194,614
: PRIOR FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: 60/195,063
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,066
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,067
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,068
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,069
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,070
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,510
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/219,855
: PRIOR FILING DATE: 2000-07-21
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 186
: SOFTWARE: CuroSeqList version 0.1
: SEQ ID NO 29
: LENGTH: 2551
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (779) .. (2503)
: US-10-174-333-29

```

Alignment Scores:

Pred. No.:	0	Length:	2551
Score:	2984.00	Matches:	574
Percent Similarity:	99.83%	Conservative:	0
Best Local Similarity:	99.83%	Mismatches:	1
Query Match:	99.83%	Indels:	0
DB:	13	Gaps:	0

US-09-927-267-1 (1-575) x US-10-174-333-29 (1-2551)



QY	MeSerGlnSPThrLysValIysThThGlnSerSerProProAlaProSerLysAla	20
Db	ATGAGCCAGAGACACCAAGTGAACAACAAGATCCAGTCCCCAGCCCATCCAGGCC	70
QY	ArgLysLeuLeuProValLeuAspProSerGlyAspTyrTyrTyrTrpPheAsnThr	40
Db	AGGAAGTTGTGCTGCTGCTGAGCCCAATCTGGGAGTACTACTAGTGGTGTGACACA	130
QY	MetValPheProValMetTyrAsnLeuIleIleLeuValCysArgAlaCysPheProAsp	60
Db	ATGGTCTTCCAGATCATGATATMACTCATCATCTCTGTGGCAAGAGCTGCTCCGAC	190
QY	LeuGlnHisGlyTyrLeuValAlaTriPheValLeuAspTyrTrpSerAspLeuLeuTyr	80
Db	TTGAGACACGGATTACTGTGGTGGCTGTGTGTGTGTGACTACACAGAGTACTGTATAC	250
QY	LeuLeuAspMetValValArgPheHisThrGlyPheLeuGlnGlnGlyIleLeuValVal	100
Db	CTACTAGACATGATGGTGGTCCGCTTCCACACAGAGATTCTTGGAACAGGGGATCTGTGGTGG	310
QY	AspLysGlyAlaGlyIleSerSerArgTyrValArgThrTrpSerPhePheLeuAspLeuAla	120
Db	GACAAAGGTAGAGACTCGAGTCGTACGCTTGACCTGGACATTTCTTGTGAGCTGACT	370
QY	SerLeuMetProThrAspValValTyrValArgLeuGlyProHisTrpProThrLeuArg	140
Db	TCCCTGATGCCACAGATGTGTCTACGTGGGCTGGGCGCCGACACACCCCTGAGG	430
QY	LeuAsnArgPheLeuArgAlaProArgPheGlnAlaPheAspArgThrGluThrArg	160
Db	CTGAACGGCTTTCTCCGGCGCCCGGCTCTTGAGGGCTTGACCCGACAGACCGCGC	490
QY	ThrAlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePheValIle	180
Db	ACAGCTTACCCAAATGCTCTTCGATTCGACAGCTGATGCTTTCATTTTGTGCTATC	550
QY	HisTrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGlyPheGlyArgAspAla	200
Db	CATTGGAACAGTGTCTACTACTTGTCCCTTATCCGGTACTCGGGCTTGGGGCGTGAACA	610
QY	TrpValTyrProAspProAlaGlnProGlyPheGluArgLeuArgArgGlnTyrLeuTyr	220
Db	TGGGTGTACCCGGACCCCGCGAGGCTGGCTTTAGAGGCTCGGGCGGCACTACTGTAT	670
QY	SerPheTyrPheSerThrLeuIleLeuThrThrValGlyAspThrProProProAlaArg	240
Db	AGCTTTTACTTCTCACCGCTGACTACTGACTACAGTGGGCGGATACACCCGCCAGCCAGG	730
QY	GluGluGluTyrLeuPheMetValGlyAspPheLeuAlaValMetGlyPheAlaThr	260
Db	GAAAGAGAGTACTCTTATAGTGGGCACTTCTGCTGGCGGTATGGATTGGCAACC	790
QY	IleMetGlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaAlaPheTyr	280
Db	ATCATGGGTAGATAGATGCTGTGTACTTACAAACATGAACACGTGGAGATGGCGCTTTTAC	850
QY	ProAspHisAlaLeuValLysLysTyrMetLysLeuGlnHisValAsnArgLysLeuGlu	300
Db	CCAGATCATGCACTGCTGTGAAGAATGAACTGACGACACGTCAACCCGCAAGCTGGAG	910
QY	ArgArgValIleAspTrpTyrGlnHisLeuGlnIleAsnLysLysMetThrAsnGluVal	320
Db	CGGCAAGTATTGACTGTGATGAGACCTGCGAGATCAACAAAGATATGCCAACAGGATA	970
QY	AlaIleLeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSerValHisLeu	340
Db	GCCATCTTACAGCACTTGCCTGAGCGGCTGGCGGCAAGATGGCTGTGTCTGTGCACTTG	1030
QY	SerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGlnGluLeu	360
Db	TTCACCTCTGAGCCGGGATGCAGATCTTTTGAGAACTGTGAAGGCCAGGCTGTGGAGAGCTG	1090
QY	ValLeuLysLeuGlnProGlnThrTyrSerProGlyGluTyrValCysArgLysGlyAsp	380

```

Db      1091 GTGCTAGAGCTGCAGCCGCCAGACCTTACTCACCGAGGTGAATATCTATTCGCCGCAAGAGAGAC 1150
QY      381 ILLEGYLGNLMETRYTIIELIETARGUIGLHLEUALAVAIAlaaspapgy 400
DB      1151 ATTGGCCAAAGATGTACATCATCTCCAGAGAGGTCACTGGCCGTGGGGAGATGATGT 1210
QY      401 ILETGINTYRALVALLEUGIYIAGIYLEUTYRPhEgylulleserIleasn 420
DB      1211 ATCACACAGTATCTGTCTGCTCGGTGCAGGGCTCTACTTTGGGAGATCACATCATCAAC 1270
QY      421 ILEYSIYASNETSERGIYASNAARGYTHAlaasnIleYserLeuGIYRser 440
DB      1271 ATCAAAGGAAACATGTCTGGGAACCCCGCACAAACCAATCAAAGACCTTAGGTATTCCA 1330
QY      441 ASPLENPHEYSLEUSERIYSGIUNASPLEUARGIUVALLEUSERGIUTYRPROGINAla 460
DB      1331 GACCTATTCTGCTGTGAGCAAGAGGACCTGGGAGGTGTGTGAGCGATATCCAAAGCA 1390
QY      461 GLCTHRIIEMETGUGIULYSGIYARGIULILEULEULYSMETASNYLSLEASPVAl 480
DB      1391 CAGACCTATCTGAGAGAGAAAGACCGTGAATCTGCTGTGAATAATGACAAAGTTGGAGCTG 1450
QY      481 ASNALAGIUALAAGIULILEALALEUGINGIUALATHRIGUSERATGUAARGIYLeu 500
DB      1451 AATGCTAGGCAAGTGTGAGATCGCCCTGCAGAGGCCCAAGATGCCCGCTACAGAGGCTTA 1510
QY      501 ASPGINGLINLEUSPAPLEUNGINTHLYPHEALARGLEULEUAlagIuleuGIUSer 520
DB      1511 GACACGAGGTGTGATGTATCTACAGACCAAGTTGCTGCTGCTGCGGTGAGCTGGAGTCC 1570
QY      521 SERALALEULYSIIETATYRArgIleGIUARGLEUGIUTYRGINTHRARGIUTYRPro 540
DB      1571 AGCCACTTAAAGATGCTTACCGCATTAAGACGGTGGAGTGGCAGATCCAGAGTGGCCA 1630
QY      541 METPROGLINASPLEUALAGIUALAASPAPSGIULYGLNUPROGIUGIULYTHRSerLYs 560
DB      1631 ATGCCGAGGACCTGGCTGTGAGCTGATGACGAGGGGTAGAGCTGAGGAGGAACTTCCAAA 1690
QY      561 ASPGLUGIULYATGAlaserGINGLIULYPROROLYPROGIU 575
DB      1691 GATGAAGAGGCGCAGGGCCAGCCACAGAGGAGACCCCCAGGCTCCAGAG 1735

RESULT 9
US-10-207-951-1
/ Sequence 1, Application US/10207951
/ Publication No. US20030013156A1
/ GENERAL INFORMATION:
/ APPLICANT: KARL GUEGLER et al.
/ TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
/ TITLE OF INVENTION: AND USES THEREOF
/ FILE REFERENCE: CL000663CON
/ CURRENT APPLICATION NUMBER: US/10/207,951
/ CURRENT FILING DATE: 2002-07-31
/ PRIOR APPLICATION NUMBER: 09/735,932
/ PRIOR FILING DATE: 2000-12-14
/ PRIOR APPLICATION NUMBER: 60/211,223
/ PRIOR FILING DATE: 2000-06-13
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1758
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) .. (1758)
/ OTHER INFORMATION: n = A,T,C or G
US-10-207-951-1

Alignment Scores:      0      Length: 1758
Pred. No.:

```

Score: 2976.00 Matches: 572  
 Percent Similarity: 99.83% Conservative: 2  
 Best Local Similarity: 99.48% Mismatches: 1  
 Query Match: 99.57% Indels: 0  
 Gaps: 0  
 US-09-927-267-1 (1-575) x US-10-207-951-1 (1-1758)

QY 1 MetSerGlnAspThrLysValLysThrThrGluSerSerProProAlaProSerLysAla 20  
 Db 11 ATGACCAAGGACACCAAGGAGCAACAGAGTCCAGTCCGCCAGCCCAATCCAAAGCC 70  
 QY 21 ArgLysLeuLeuProValLeuAspProSerGlyAspIlyrTyrTyrTrpLeuAsnThr 40  
 Db 71 AGGAAGTGTCTGCTGCTGCTGCAACCATCTGGGAGATTACTACTACTGCTGGCTGAACA 130  
 QY 41 MetValPheProValMetTyrAsnLeuLeileuValCysArgAlaCysPheProasp 60  
 Db 131 ATGCTCTTCCAGCATGATATACCTCATCATCTGCTGTCAGAGCCTGCTTCCCGAC 190  
 QY 61 LeuGlnHisGlyTyrLeuValAlaIlePheValLeuAspIlyrThrSerAspLeuLeuTyr 80  
 Db 191 TTGACAGACAGGTTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250  
 QY 81 LeuLeuAspMetValValArgPheHisThrGlyPheLeuGlnGlyIleLeuValVal 100  
 Db 251 CTACTAGACATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310  
 QY 101 AspLysGlyArgIleSerSerArgTyrTyrValArgThrTyrPhePhePheLeuAspLeuAla 120  
 Db 311 GACAAAGGATGAGATTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370  
 QY 121 SerLeuMetProThrAspValValIleTyrValArgLeuGlyProHisThrProThrLeuArg 140  
 Db 371 TCCCTGAGTCCCAAGAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430  
 QY 141 LeuAsnArgPheLeuArgAlaProArgLeuPheGlnAlaPheAspArgThrGluThrArg 160  
 Db 431 CTGAACGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490  
 QY 161 ThrIleTyrProAsnAlaPheArgIleAlaIleLeuMetLeuTyrIlePheValValIle 180  
 Db 491 ACAGCTTACCCAAAGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
 QY 181 HisTrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGlyPheGlyArgAspAla 200  
 Db 551 CATGGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610  
 QY 201 TrpValTyrProAspProAlaGlnProGlyPheGlnArgLeuArgGlnTyrLeuTyr 220  
 Db 611 TGGGTGTACCCGAGCCCGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670  
 QY 221 SerPheTyrPheSerThrIleuIleLeuThrThrValGlyAspThrProProProAlaArg 240  
 Db 671 AGCTTACTTCTTCCAGCTGATACTGATCACTGAGGCGGATTAACCGCCGCCAGCGAG 730  
 QY 241 GlnGlnGlnIleuTyrLeuPheMetValGlyAspPheLeuLeuAlaValMetGlyPheAlaThr 260  
 Db 731 GAAGAAGAGTACCTTCTCATGTGTGGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 790  
 QY 261 IleMetGlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaAlaPheTyr 280  
 Db 791 ATCATGTGGTGTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850  
 QY 281 ProAspHisAlaLeuValLysIleTyrMetLysLeuGlnHisValAsnArgLysLeuGln 300  
 Db 851 CCAGATATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910  
 QY 301 ArgArgValIleAspTyrTyrGlnHisLeuGlnIleAsnLysLysMetThrAsnGlnVal 320  
 Db 911 CGGGAGATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970  
 QY 321 AlaIleLeuGlnHisLeuProGlnArgLeuArgAlaGlnValAlaValSerValHisLeu 340

Db 971 GCCATCTTACAGCACTTCCCTGAGCGGCTGCGGAGAGAGTGTGTGTCTGTGCACCTG 1030  
 QY 341 SerThrLeuSerArgValGlnIlePheGlnAsnCysGlnAlaSerLeuLeuGlnLeu 360  
 Db 1031 TCCACTGTGAGCCGGGTGCAGATCTTTCAGAACTGTGAGGCGCAGCTGTGTGAGAGCTG 1090  
 QY 361 ValLeuLysLeuGlnProGlnThrTyrSerProGlyIleTyrValCysArgLysGlyAsp 380  
 Db 1091 GTGCTGAAGCTGACCCCGACCTTACACAGGTGATATGTATGCTGCGCAAGAGAGC 1150  
 QY 381 IleGlyGlnGlnMetTyrIleIleArgLysGlnGlnLeuAlaValAlaAspAspGly 400  
 Db 1151 ATTGGCCAAAGATGTATATATCATCCGAGAGGTCAACGCGCTGTGTGTGAGATATGT 1210  
 QY 401 IleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGlnIleSerIleLeuAsn 420  
 Db 1211 ATCACACAGTATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270  
 QY 421 IleLysGlyAsnMetSerGlyAsnArgArgThrAlaAsnIleLysSerLeuGlyTyrSer 440  
 Db 1271 ATCAAAGGAAACATGTCTGGGAAACCGCCGCAACCAACATCAAGAGCTTAGTTATCA 1330  
 QY 441 AspLeuPheCysLeuSerLysGlyAspLeuArgGlnValLeuSerGlyTyrProGlnAla 460  
 Db 1331 GACCTATTCTGCTGAGCAAG 1390  
 QY 461 GlnThrIleMetGlnGlnLysGlyArgGlnIleLeuLeuLysMetAsnLysLeuAspVal 480  
 Db 1391 CAGACCATCATGAGGAG 1450  
 QY 481 AsnAlaGlnAlaAlaGlnIleAlaLeuGlnGlnAlaThrGlySerArgLeuArgGlyLeu 500  
 Db 1451 AATGCTAGGAGAGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1510  
 QY 501 AspGlnGlnLeuAspAspLeuGlnThrLysPheAlaArgLeuLeuAlaGlnLeuGlySer 520  
 Db 1511 GACCAAGAGAGCTGAGTGTATCTACAGACCAAGTTTCTGCTGCTGCTGCTGCTGCTGCT 1570  
 QY 521 SerAlaLeuLysIleAlaTyrArgIleGlnArgLeuGlnTyrPheGlnThrArgGlnTyr 540  
 Db 1571 AGCCCACTTAAAGATGCTTACCGCATTAACAGCGCTGAGTGTGAGACTGAGAGAGG 1630  
 QY 541 MetProGlnLysLeuAlaGlnAlaAspAspGlnGlnIleProGlnGlnGlyThrSerLys 560  
 Db 1631 ATGCCCAAGAGAGCTGCTGAGCTGAGTGAACAGAGGTGAGCTGAGAGAGAACTTCCAA 1690  
 QY 561 AspGlnGlnGlyArgAlaSerGlnGlnGlyProProGlyProGln 575  
 Db 1691 GATGAAAGAGGAGGAGGCGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1735

RESULT 10  
 US-09-842-758-27  
 Sequence 27, Application US/09842758  
 Publication No. US20030083244A1  
 GENERAL INFORMATION:  
 APPLICANT: Vernet, Corine A. M.  
 APPLICANT: Fernandes, Elma R.  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Shinkets, Richard A  
 APPLICANT: Malyankar, Uriel M  
 APPLICANT: Boldog, Ferenc L.  
 APPLICANT: Zerkusen, Bryan D  
 APPLICANT: Spytek, Kimberly A  
 APPLICANT: Majumder, Kumud  
 APPLICANT: Tcherner, Velizar T  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Patlurajan, Meera  
 APPLICANT: Burgess, Catherine E  
 APPLICANT: Gangoli, Bha A  
 APPLICANT: Smitson, Glenda  
 APPLICANT: Rastelli, Luca  
 APPLICANT: MacDougall, John R



QY 458 ProGluAlaGlnThrIleMetGluGlyArgGluIleLeuLeuLysMetAsnLys 477  
 Db 1434 CCACAGACACAGACCATCATGAGGAGAAAGACGTGAGATCTCTGTAATAAGCAAG 1493  
 QY 478 LeuAspValAsnAlaGluAlaGluIleAlaLeuGlnGluIleThrGluSerArgLeu 497  
 Db 1494 TTGAGCGTGAATCTGAGGACGTGAGATGCTGCGAGAGGACCAAGAGTCCCGACTA 1553  
 QY 498 ArgGlyLeuAspGlnGlnLeuAspLeuGlnThrLysPheAlaArgLeuLeuAlaGlu 517  
 Db 1554 CGAGGCTGACACAGACGTGATGATCTACAGACCAAGTTCTGCTCCCTCGGCTGAG 1613  
 QY 518 LeuGluSerSerAlaLeuLysIleAlaIYArgIleGluArgLeuGluThrGlnThrArg 537  
 Db 1614 CTGAGATCCAGCGCACTTAAGATTGCTTACCGCATTAACCGCTGAGTGGCAGACTCGA 1673  
 QY 538 GluTrpProMetProGluAspLeuAlaGluAlaAspAspGluGlyGluProGluGluGly 557  
 Db 1674 GAGTGGCCAAATGCCAGAGACCTGAGGCTGAGGCTGATGACGAGGAGTGAAGCTGAGAGGGA 1733  
 QY 558 ThrSerLysAspGluGluGlyArgAlaSerGlnGluGlyProProGlyProGlu 575  
 Db 1734 ACTTCCAAGATGAAGAGAGGAGGCGCCAGCCAGAGAGGAGCCCGCAAGTCCAGAG 1787

## RESULT 11

US-10-174-333-27  
 ; Sequence 27, Application US/10174333  
 ; Publication No. US20040029220A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vermet, Corine A.M.  
 ; APPLICANT: Fernandes, Elma R.  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Malyankar, Uriel M.  
 ; APPLICANT: Boldog, Ferenc L.  
 ; APPLICANT: Zethusen, Bryan D.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Majumder, Kumud  
 ; APPLICANT: Tchernev, Velizar T.  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Patutajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Gangolli, Esha A.  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: MacDougall, John R.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Groesse, William M.  
 ; APPLICANT: Szekeles, Edward S.  
 ; APPLICANT: Alsobrook, John P.  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Guo, Xiaojia (Sasha)  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Zhong, Mei  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 15966-783 CIP1  
 ; CURRENT APPLICATION NUMBER: US/10/174.333  
 ; PRIOR FILING DATE: 2002-06-18  
 ; PRIOR APPLICATION NUMBER: 60/193,664  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 60/194,614  
 ; PRIOR FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: 60/195,063  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/195,066  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/195,067  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/195,068  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/195,069  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/195,070  
 ; PRIOR FILING DATE: 2000-04-06

QY PRIOR APPLICATION NUMBER: 60/195,510  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/219,855  
 ; PRIOR FILING DATE: 2000-07-21  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: CuroSeqList version 0.1  
 ; SEQ ID NO 27  
 ; LENGTH: 1835  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (54)..(1787)  
 ; US-10-174-333-27  
 Alignment Scores:  
 Pred. No.: 0 Length: 1835  
 Score: 2957.50 Matches: 575  
 Percent Similarity: 99.48% Conservative: 0  
 Best Local Similarity: 98.48% Mismatches: 0  
 Query Match: 98.95% Indels: 3  
 DB: 13 Gaps: 3  
 US-09-927-267-1 (1-575) x US-10-174-333-27 (1-1835)  
 QY 1 MetSerGlnAspThrLysValLysThrThrGluSerSerProProAlaProSerLysAla 20  
 Db 54 ATGAGCCAGGACACCAAGGTGAAGAACAGAGTCCAGGCCCGCCAGCCCATCCAGAGGCC 113  
 QY 21 --ArgLysLeuLeuProValLeuAspProSerGlyAspTyrTyrTyrTrpTrpLeuAsn 39  
 Db 114 AGGAGGAAGTGTCTCCCTGCTGAGACCCATCTGGGGATTACTACTGAGGCTGAAC 173  
 QY 40 ThrMetValPheProValMetTyrAsnLeuIleIleValCysArgAlaCysPhePro 59  
 Db 174 ACAATGCTCTCCCGATCATGTAATACCTCATCCTCGTGTGAGGCGCTTCCCTCC 233  
 QY 60 AspleuGlnHISGlyTyrLeuValAlaTrpLeuValLeuAspTyrThrSerAspleuLeu 79  
 Db 234 GACTTGCAGCAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 293  
 QY 80 TyrLeuLeuAspMetValAlaArgPheHisThr---GlyPheLeuGluGlnGlyIleLeu 98  
 Db 294 TACCTACTAGACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353  
 QY 99 ValValAspLysGlyArgIleSerSerArgTyrValArgThrTrpSerPhePheLeuAsp 118  
 Db 354 GTGATGACACAGGAGTATCTGAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 413  
 QY 119 LeuAlaSerLeuMetProThrAspValValIYArgLeuGlyProHisThrProThr 138  
 Db 414 CTGGCTTCCCTGAGTCCACAGATGTGCTTACAGCTGCGGCGGCCGACACACACCCACC 473  
 QY 139 LeuArgLeuAsnArgPheLeuArgAlaProArgLeuPheGluAlaPheAspArgGln 158  
 Db 474 CTGAGGCTGAACCGCTTCTCCGCGGCGGCCGCTTCCGAGGCTTGAAGCGGACAGAG 533  
 QY 159 ThrArgThrAlaIYProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePheVal 178  
 Db 534 ACCCGACAGCTTACCCCAATGCTTTCGATGCAATGCAATGCAATGCAATGCAATGCAAT 593  
 QY 179 ValIleHISTrpPanserCysLeuTyrPheAlaLeuSerArgTyrLeuGlyPheGlyArg 198  
 Db 594 GTCAATCATGGAACAGCTGCTTACTTTCCTTACCTCCGCTTACCTGCGGCTTGGGGCT 653  
 QY 199 AspAlaTrpValIYProAspProAlaGlnProGlyPheGluArgLeuArgArgGlnTyr 218  
 Db 654 GAGCATGGGTGATCCCGGAGCCCGGCGAGCTGCTTGAAGCGGCTGCGGCGGCGGAGTAC 713  
 QY 219 LeuTyrSerPheTyrPheSerThrLeuIleLeuThrThrValGlyAspThrProProPro 238  
 Db 714 CTCTATAGCTTTTACTTCTCCAGCTGATCTGACTGACTGACTGACTGACTGACTGACTGACT 773

QY 239 AlaArgLugluGluTyrLeuPheMetValGlyAspPheLeuValAlaMetGlyPhe 258  
 Db 774 GCCAGGGAAGAAGAGTACCTTCAATGATGGGCACTTCCTGGCGGCTGATGGTTTC 833  
 QY 259 AlaThrIleMetGlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAla 278  
 Db 834 GCCACCATCATGGTAGATAGCTCTGTCACTTCAACATGAACACTGCAGATCCGGCT 893  
 QY 279 PheTyrProAspHisAlaLeuValLysTyrMetLysLeuGlnHisValAsnArgLys 298  
 Db 894 TTCTAACCATCATGATGCACTGGTGAAGAAGTACAGAACTGCAGCAGCTCAACCGCAAG 953  
 QY 299 LeuGluAlaGluValIleAspTyrTyrGlnHisLeuGlnIleAsnLysLysMetThrAsn 318  
 Db 954 CTGGAGCGCGGAGTATGACTGGTATCAGCACTGCAGATCAACAAAGAATGACCAAC 1013  
 QY 319 GluValAlaIleLeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSerVal 338  
 Db 1014 GAGGTAGCATCTTACAGCACTTGGCTGAGCGGCTGGCGGCAAGAGTGGTGTCTGTG 1073  
 QY 339 HisLeuSerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGlu 358  
 Db 1074 CACCTGTCACCTGAGCCGGGTGCAATCTTTCAGAACTGTGAGCGCAGCTGCTGGAG 1133  
 QY 359 GluLeuValLeuLysLeuGlnProGlnThrTyrSerProGluTyrValCysArgLys 378  
 Db 1134 GAGCTGGTCTGAAGCTGAGCCCAAGCTACTACCAAGGTGAATATGATATGCCGCAAA 1193  
 QY 379 GlyAspIleGlyGlnGluMetTyrIleIleArgGluGlnLeuAlaValAlaAsp 398  
 Db 1194 GAGAGCATTTGGCCAAAGATGATACATCCAGAGGGCTCACTGGCTGGTGGCAAGT 1253  
 QY 399 AspGlyIleThrGlnTyrAlaValLeuGlnLysGlyLeuTyrPheGlyGluIleSerIle 418  
 Db 1254 GATGGATACACACAGATATGCTGTGCTGGTGCAGGGCTCTTACTTGGGAGATGACATC 1313  
 QY 419 IleAsnIleLys---GlyAsnMetSerGlyAsnArgArgThrAlaAsnIleLysSerIle 437  
 Db 1314 ATCAACATCAAAAGGTGGGAACATGCTGGGAACCGCCGACCAACCAATCAAGAGCCTTA 1373  
 QY 438 GlyTyrSerAspLeuPheCysLeuSerLysGluAspLeuArgLysValLeuSerGluTyr 457  
 Db 1374 GGTATTTCAGACTTATTTCTGCTGAGCAAGAGAGACTTCGGGAGGTGCTGACCAATAT 1433  
 QY 458 ProGlnAlaGlnThrIleMetGluGluLysGlyArgGluIleLeuLeuLysMetAsnLys 477  
 Db 1434 CCACAGACACACACATCATGAGAGAGAAAGACGTGAGATCCTGCTGAATAAGAACAG 1493  
 QY 478 LeuAspValAsnAlaGluAlaIleGluIleAlaLeuGlnLysAlaThrGluSerArgLeu 497  
 Db 1494 TTGGACGTGAATGCTGAGGAGCTGAGATGCTCTGCAAGAGGCCACAGAGTCCCGGCTTA 1553  
 QY 498 ArgGlyLeuAspGlnGlnLeuAspAspLeuGlnThrLysPheAlaArgLeuLeuAlaGlu 517  
 Db 1554 CCAAGGCTTAGACAGAGCTGATGATCTACAGACCAAGTTTGTCTGCTCCGGTGGAG 1613  
 QY 518 LeuGluSerSerAlaLeuLysIleAlaTyrArgIleGluArgLeuGluTyrGlnThrArg 537  
 Db 1614 CTGGAGTCCAGCGCATTAAGATTGCTTACCGCATTAAGACGGCTGAGGCGAGACTCA 1673  
 QY 538 GluTyrProMetProGluAspLeuAlaGluAlaAspAspGluGluProGluGluGly 557  
 Db 1674 GAGTGGCCATATGCCAGAGCTGGGCTGAGGCTGATGACGAGGGGTAGAGCTGAGAGGGA 1733  
 QY 558 ThrSerLysAspGluGluArgAlaSerGlnGluGlyProProGluProGlu 575  
 Db 1734 ACTTCCAAGATGAAGAAGGCGAGGCCAGCGAGAGAGAGCCCAAGTCCAGAG 1787

; GENERAL INFORMATION:  
 ; APPLICANT: GUEGLER, Karl et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 ; FILE REFERENCE: AND USES THEREOF  
 ; FILE REFERENCE: C0000663  
 ; CURRENT APPLICATION NUMBER: US/09/735,932  
 ; CURRENT FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 3  
 ; LENGTH: 10989  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-735-932-3  
 Alignment Scores:  
 Pred. No.: 5,45e-259 Length: 10989  
 Score: 2266.00 Matches: 573  
 Percent Similarity: 33.01% Conservative: 0  
 Best Local Similarity: 33.01% Mismatches: 2  
 Query Match: 75.81% Indels: 1163  
 Gaps: 5  
 DB:  
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 QY 1 MetSerGlnAspThrLeuValLysThrThrGluSerSerProGluAlaProSerLysAla 20  
 Db 3000 ATGAGCCGAGACACCAAGTGAAGACACAGATGCAATCCCGAGCCCATCAAGGCC 3059  
 QY 20 ----- 20  
 Db 3060 AGGTGAAGTCCGTGCTCCCTGTGTGGAGTCTCTCATTCCTTGTGTGCCAGATC 3119  
 QY 21 ----- Argly 22  
 Db 3120 ACACATCAGCTTGAATGCTGATGAATTAATGAACAGACCTTCTTCTTAAGGAA 3179  
 QY 22 sLeuLeuProValLeuAspProSerGlyAspTyrTyrTyrTyrPleuAsnThrMetVal 42  
 Db 3180 GTTGTGCTGCTGCTGAGACCATCTGGGATTAATCACTGCTGTGCTGAGACATATGCT 3239  
 QY 42 lPheProValMetTyrAsnLeuIleIleLeuVal----- 53  
 Db 3240 CTCCCAAGTCAATTAATCACTCATCTCTGTCGAGATGAGATGAGAGCGGTCTTAAGG 3299  
 QY 53 ----- 53  
 Db 3300 AGGGCTGAGAGCCCAAAAGAGACTTAAGAGAGTCAAGAGAGGCGACACCTTGGT 3359  
 QY 53 ----- 53  
 Db 3360 GGGGAGAGAGAGCAATTCATGGAGAGGCTGAGAGGAGGTTAAGGGCCCTGGGGA 3419  
 QY 54 ----- CysArgly 56  
 Db 3420 GAGCCTGACACAGAGGGTCCCTTAATCAATCATGCTTAACCTGCGCTGAGAGG 3479  
 QY 56 aCysPheProAspLeuGlnHisGlyTyrLeuValAlaTyrPleuValLeuAspTyrThrSe 76  
 Db 3480 CTGCTTCCCGCATGTCACACAGGTATATGTGGGCTGTGGTGGTCTGAGACTACAGAG 3539  
 QY 76 rAspLeuLeuTyrLeuLeuAspMetValAlaArgPheHisThr----- 90  
 Db 3540 TGAATGCTTAATCACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3598  
 QY 90 ----- 90  
 Db 3599 GGAATGACCTTTTGTCCACATTCCTCTTAAGATAGCACTTAAGAGTAACAAGAA 3658  
 QY 90 ----- 90  
 Db 3659 AGGCAACCCCAAGCTGTGAGACCTTGGGTGCTGTATGCTGAGACATCCCAAGTCT 3718



QY	90	-----	90	QY	306	-----	306
Db	3719	CACCCGGAAGCGGAGAGAGATTAGCTGCTCCACTCTGCTTCCAGACAGTCTC	3778	Db	4799	TGGAAGAGTGGGTGAAGAAGGCAATCCCCCTTGAAATGCTCAGCAACAGATCATTTG	4858
QY	90	-----	90	QY	306	-----	306
Db	3779	CCTGGCTGCTGGGAGCTCATGCTCAGCCCAAGCTTGATCAGCAGTCCGCTCC	3838	Db	4859	GCTACTATGTGATTCATCTGTGAGCTGAACAAAGAGAGTCAACAAGTTGGGAA	4918
QY	91	-----	91	QY	306	-----	306
Db	3839	TACCGGCTCCCTCTCCCGAGATTCTTGAGACAGGSCATCTGGTGTGAGCAAGGTTAG	3898	Db	4919	GTAGACAGAGGATCCCGACAGAGAGAGGAGCCCTTGGTGGCTGAGGTAAAGGTAGG	4978
QY	104	gllleSerSerArgIYrValArgThrTyrSerPhePheLeuAspLeuAlaSerLeuMetPr	124	QY	306	-----	306
Db	3899	GATCTCGAGTCCCTAGCTGCTGAGCAGCTGAGGATTTCTTTCGACCTGCTTCCCTGATGCC	3958	Db	4979	GGTGAACAAGACATCATCTGATTGGTGGTGAAGCTTGATAGAGGTGAAGGTT	5038
QY	124	oThrAspValValTyrValArgLeuGlyProHisThrProThrLeuArgLeuAsnArgPh	144	QY	306	-----	306
Db	3959	CACAGATGTGTCTTACCTGCTGAGGCTGAGCCCGACACACACCCTGAGGCTGAACCGCTT	4018	Db	5039	ATGTAAAGTGTAGAGGTGTCTATGCCCTGAAACAGTAATCCAACTGTCAAGTACTTC	5098
QY	144	eLeuArgAlaProArgLeuPheGluAlaPheAspArgThrGluThrArgThrAlaTyrPr	164	QY	306	-----	306
Db	4019	TCTCGCGCGCGCCCGCTCTTGAAGGCTTGCACCGCACAGAGACCCGACAGCTTACCC	4078	Db	5099	CCATGACCCCTGTAGATCTAGTATGCTGAGGATTTCTGGCTGAGCTGAGCTGACCTC	5158
QY	164	oAsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePheValValIleHisTyrAsnSe	184	QY	306	-----	306
Db	4079	AAATCCCTTTCGATTCGACCTGACCACTGATGCTTACATTTTTCGTCATCCATTGGAACAG	4138	Db	5159	GAAAGAGGATGAGAGGACGACATTAAGGCTGTGAAGAAATGGCACTGCTCTACT	5218
QY	184	rCysLeuTyrPheAlaLeuSerArgTyrLeuGlyPheGlyArgAspAlaTyrPrValTyrPr	204	QY	307	-----	307
Db	4139	CTGCTTATACCTTGGCTTACCTCCCGGACCTGAGGCTTGGGCGCTGAGCAGATGGGTGTACC	4198	Db	5219	CTCAGGTATCAGACCTTCAGATCAACAGAAAGATGACCAACAGAGTACCTTCAACG	5278
QY	204	oAspProAlaGlnProGlyPheGluArgLeuArgArgGlnTyrLeuTyrSerPheTyrPh	224	QY	325	HisLeuProGluArgLeuArgAlaGluValAlaValSerValHisLeuSerThrLeuSer	344
Db	4199	GGACCCCGCGAGCTGCTTGAAGCGCTGAGCGGCCAGTACCTTACCTTACCTTTTACTT	4258	Db	5279	CATTGCTTGAAGCGCTGCGGAGAGAGTGGCTGTCTGTGACCTGTCCACTCTGAGC	5338
QY	224	eSerThrLeuIleLeuThrThrValGlyAspThrProProProAlaArgIleGluGluTyr	244	QY	345	ArgValGlnIlePheGlnAspCysGlnAlaSerLeuLeuGluIleValIleuValLeuLysLeu	364
Db	4259	CTCACGCTGATACGACTACAGTGGCGATACACCGCGCCGACGACGAGGAAGAAAGATA	4318	Db	5339	CGGCTGAGATCTTTCAGAACTGTGAGCGCAGCTGCTGAGAGAGCTGTGTGAAGCTG	5398
QY	244	rLeuPheMetValGlyAspPheLeuLeuAlaValMetCysPheAlaThrIleMetGlySe	264	QY	365	GlnProGlnThrTyrSerProGlyGluTyrValCysArgLysGlyAspIleGlyGlnGlu	384
Db	4319	CCTCTTACCTGCTGGCGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4378	Db	5399	CAGCCCGAGACTTACTCAACAGAGTGAATATATATATATATATATATATATATATATAT	5458
QY	264	rMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaAlaPheTyrProAspHisAla	284	QY	385	MetTyrIleIleArgGluGluGluLeuAlaValValAlaAspAspGlyIleThrGlnTyr	404
Db	4379	CATGAGCTCTGTCACTTACCAACATGAAACATGCACTGCAAGATGCGCTTTCACCAATTCATGC	4438	Db	5459	ATGTACATCATCCAGAGGCTCAACTGCGCTGTGGCAAGTATGATGATCATCAACATCA	5518
QY	284	AlaValLysLysTyrMetCysLeuGlnHisValAsnArgLysLeuGluArgArgValIle	304	QY	405	AlaValLeuGlyAlaGlyLeuTyrPheGlyGlnIleSerIleIleAsnIleLys-----	422
Db	4439	ACTGCTGAAGAAGTACATGAAGCTGACAGCATGCAACGCAAGCTGAGCGGCAAGTTAT	4498	Db	5519	GCTGTCTCGTGCAGGCTCTTACTTGTGGAGATGACATCATCAATCAATCA-----	5577
QY	304	eAspTyr-----	306	QY	422	-----	422
Db	4499	TGACTGTGAGAAAGCGGGCTTCCAGACACAGACAGGACCAAGTATGATGAAACT	4558	Db	5578	GTATCCAGTATTTGTTCCAGGAGCAAGGATGGGTGAGGGGAGCAACGACAGACCC	5637
QY	306	-----	306	QY	422	-----	422
Db	4559	GAGGAGGTAACTGGGTCTTATAGCTGTGAGACAGCAAGGCTGTCAAAATGTAGCA	4618	Db	5638	AGTGTGGAGCAGATAGTACTTCAAGCTTAACTTGTATGAGAAACCTGGCCCTTC	5697
QY	306	-----	306	QY	422	-----	422
Db	4619	TTGACCGGTGGTTGTGCTGGGCTTGAAAAAGGAACCTTTTCAACTGAGGAA	4678	Db	5698	TCTGAGTCACTAATGCTCAGAGAAAAAACAACATAGAGATCCATTCCTCGAGAG	5757
QY	306	-----	306	QY	422	-----	422
Db	4679	TCAGACTTGGGAGGCGGTAGGTAAAGACTGATAGGAGAGAGCTCATACTCAAAAA	4738	Db	5758	AAGCTGAGCAAGGCGCAGTGAACAGGGTGGGTTGTGGAAGAGAGACTAGACTTGTCTG	5817
QY	306	-----	306	QY	422	-----	422
Db	4739	AGGATAATATGAGACCGAGGAATGGGAAGTGCACATGCTGCTGATGAGGCTCAGAAAGCTC	4798	Db	5818	TGATATTACCTTGAAGACCAATAGACTAGTGACAGTATGATGATATATATATATAT	5877
QY	4739	AGGATAATATGAGACCGAGGAATGGGAAGTGCACATGCTGCTGATGAGGCTCAGAAAGCTC	4798	QY	422	-----	422

Db	5878	AAATAGTAATATTATTACTGCTTACTGCATCCCTTTTCTAAGTCTTCAATGATAT	5937
Qy	422	-----	422
Db	5938	TAACTCATTAATTCGGCAGCACTTCTATTAAGTAAGTACTATTCTTATCCCAATTTA	5997
Qy	422	-----	422
Db	5998	AAGATAAGAAATCAAACTCAAGAAAGTGGTAATTGCCCAAGTCGACAGATATAC	6057
Qy	422	-----	422
Db	6058	ACATGTGGATGATGGAAAAACAACCTTTTACAGCCAAAGTGAAGAAAGTAGA	6117
Qy	422	-----	422
Db	6118	AGAGAAAGTTCCATTACTGACATCACTCTAGGCCAAGCAAGTACTACTACTG	6177
Qy	422	-----	422
Db	6178	GCTTGCTTTTCTCTCATCAGCCCTGTGAGTAGGAATGTATGCTTAATCAGGTA	6237
Qy	422	-----	422
Db	6238	TTAGGCATGAGTGTGCAAGCAGAAATCCTGCAATGGGGTAAAGCACTGTGATGA	6297
Qy	422	-----	422
Db	6298	CCGAAAGCTGGATGTGCTGTGCTCTCAGCATGAGGATTTCTACCTCAGGGATTCG	6357
Qy	422	-----	422
Db	6358	AAAGCTCAGACTGTGTCTCCAGATGATCCCTCAAGTCCACATCTGTATGTGATGA	6417
Qy	422	-----	422
Db	6418	TGCTGTCTGTGACTTTGGAAGTCAATTCCTATTAGGCTCAGATTATACCTA	6477
Qy	422	-----	422
Db	6478	TCCATGAGGACATATATMAAACCAATGAGTATTGTGAAATMAATGACTATGTG	6537
Qy	422	-----	422
Db	6538	AGTAGGATCCAGCGCAGTGTGGCATACAGCAAGTGTCAACAATATGATGCTCT	6597
Qy	422	-----	422
Db	6598	TTCCCTTGTCAAGTCTTCTAGCTTAAGACTTTGACATTCAGCTCACTATCTC	6657
Qy	422	-----	422
Db	6658	CCCACCATTTCTCAACACATCTTTCTAAGTCAAGAAATATCATAGCTCCCTGCT	6717
Qy	422	-----	422
Db	6718	TAAATATCTCAATAGTTTCTAGTGCCTCAGCATTAAGCCTGAACCTTCATGTGCG	6777
Qy	422	-----	422
Db	6778	TTATGAGACCCAGTGTGACCTAGATCTCCCTCTCCACCCCTCCCAACCTGTGGCT	6837
Qy	422	-----	422
Db	6838	CTGCACTGCAAGTGTACTATTTTCTGATCAACATGACTTTTCTACCCCTTC	6897
Qy	422	-----	422
Db	6898	CTCTGTCTGCTCTCTCTCTCTGCTAGATGCTCCATCCCACTGTCTCCCTCTCC	6957
Qy	422	-----	422

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Db	6958	CCTAGTACCTCCTACTCAGTTCAGTGTATGAGACTGTTCTTGCAATTCTATTAAGAA	7017
Qy	422	-----	422
Db	7018	TATCTGACTGTGATTAATTATMAAGAAAGAGTTTAAATTGGCTCAGTCTTCAGGA	7077
Qy	422	-----	422
Db	7078	TTTACGGAGCATGTGTGCTGCAATTGTCTCAGCTCTAGGAGGCTTCAAGAACTTAT	7137
Qy	422	-----	422
Db	7138	AATTGTGCAGAGCAAGGAGGAGCAGCATGTCAACGCTGAAGACAGAGCAAGG	7197
Qy	422	-----	422
Db	7198	TTGGGGAGGTGCCACACTTTCAAAACAACCAACACAGCTCTGACTCATTAATCA	7257
Qy	422	-----	422
Db	7258	AAAGCAGCATCAAGCATGAGATGCGCCCAATATCAATCACTCCACAGATCC	7317
Qy	422	-----	422
Db	7318	CACCCCAACATGGGATTAATTCATGATGATTTGGCAGACAAATATTCAAAT	7377
Qy	422	-----	422
Db	7378	TATATCTTAGACATCCCTTCTCCAGACTTCCCTAATTCCTGCTTACGGTTGTA	7437
Qy	422	-----	422
Db	7438	GGGGCTTGTGCTACCTTCCACAGCACTGATGACATGTCTTCACTGACAGCCAT	7497
Qy	422	-----	422
Db	7498	ACTGTATATATCAATTCACATATATGTGTATCTCTAGACTGTGATTTTGAAGC	7557
Qy	422	-----	422
Db	7558	AGTCACTGATACCTACCCAGATGAGCCTGTCCCAATGATGTTACTAATTAAGAA	7617
Qy	422	-----	422
Db	7618	TTATGAGCAGAAAGAGGCTCAGAAACAATATGAGTGAAGTCTGTTGAG	7677
Qy	422	-----	422
Db	7678	GAGTAAATGCCACTCCTCACCTCTCTACTACTGTCTCCCATCTCTGCCATGAGCC	7737
Qy	423	---GlyAsnMetSerGlyAsnArgArgThrAlaAsnIleLeuSerLeuGlyTyrSerAsp	441
Db	7738	ACAGGAAACATGTCTGGGAACCGCGCAGCAACATCAAGCCTAGGTATTCAGAC	7797
Qy	442	LeuPheCysLeuSerIleGlyAsnLeuArgIleValIleLeuSerGlyTyrProGlnIleGln	461
Db	7798	CTATTCTGCTGAGCAAGAGGACCTGCGGAGGTGTAGGAGATATCAACAGACACG	7857
Qy	462	ThrIleMetGlnGluIleGlyArgGluIleLeuLeuMetAsnIleLeuSerLeuAsp	481
Db	7858	ACCATCATGAGAGAGAGAGAGCTGAGATCTGCTGTAATAAGCAAGTTGACGAGAT	7917
Qy	482	AlaGluAlaIleGluIleLeuGlnGluIleThrGluSerArgLeuArgGlyLeuAsp	501
Db	7918	GCTGAGCAGCTGAGATTCGCCCTGCGAGGAGGACAGAGATCCGAGCTACGAGGCTAGAC	7977
Qy	502	GlnGlnLeuAspSerLeuGlnThrIlePheAlaArgLeuLeuAlaIleLeuGlnIleSer	521
Db	7978	CAGCAGCTGATGATCTTACAGAACAAATTGCTGCTGCTCTGCTGAGCTGAGTCCAGC	8037
Qy	522	AlaLeuIleIleAlaIleArgIleGlyArgLeuGlnIleProIleThrArgIleTyrProMet	541
Db	8038	GCATTAAATGCTTACCGCATTTGAACGCTGGAATGGAGACTCGAAGTGGCCATG	8097

QY	Db	QY	Db
542	8098	562	8158
<pre> TGGTGAAPLeuAlaGlnAlaAspAspGlnGlyGluProGlnGlnGlnGlyThrSerLysasp       CCCAAGAGCTCGCTGAGGCTGATACAGAGGTAGAGCTGAGAGAGGAACTTCCAAAGT </pre>	815	<pre> GlnGlnGlnGlyAlaSerGlnGlnGlyProProGlyProGln       GAAAGAGGCGAAGGCCAGCGAAGGAGACCCCGAGGTCGAGG </pre>	8199

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RESULT 13
US-10-207-951-3
; Sequence 3, Application US/10207951
; Publication No. US20030013156A1
; GENERAL INFORMATION:
; APPLICANT: Karl GUEGLER et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
; TITLE OF INVENTION: AND USUS THEROOF
; FILE REFERENCE: C10006630N
; CURRENT APPLICATION NUMBER: US/10/207,951
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/735,932
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/211,223
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10989
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-207-951-3

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Alignment Scores:		
Pred. No.:	5,456-259	Length: 10989
Score:	2266.00	Matches: 573
Percent Similarity:	33.01%	Conservative: 0
Best local Similarity:	33.01%	Mismatches: 2
Query Match:	75.81%	Indels: 1163
DB:	15	Gaps: 5

QY	1	MetSerGlnAspThrLysValIleThrThiGlnSerSerProProAlaProSerIleVala	20
	3000	ATGAGCCAGAGACACCAAGTGAAGACAAGAGTCAAGTCCCAAGCCCATCCAGAGCC	3055
QY	20	-----	20
Db	3060	AGGTAGAAAGTCTGGTCCCTTGTGTGGAGTCTCTCTCATTTCTTGGTCCCAAGC	3115
QY	21	-----	21
		Argly	22
	3120	ACAACCTACAGCTTGAATGCTGGTGAATAAATGAACAGACTTTCTTTCTTAACAGAA	3175
QY	22	StenleuProValIleuAspProSerGlyAspIYrTYrTYrTriPLeuAsnThwEva	42
	3180	GTTGTGCTCTGCTCCCGAGCCCATCTGGAGATTCTACTACTGGTGGCTGAACAACATGAT	3235
QY	42	1PheProValMetTYrAsnLeuIleIleuVal-----	53
Db	3240	CTTCCCACTCATGTATAACTCATCATCTCTGTGTGAGGTATGGAGGGGTCTAAGGG	3295
QY	53	-----	53
Db	3300	AGGGGCTGGAAAGCCAAAAGAGACTAAAGAGAGCTAAGAGAGAGAGGACAGACCTTGAT	3355
QY	53	-----	53
		CysArgAl	56
	3360	GAGGAGAGAGAGCAATTTCCATGGAGAGGCTCTGAGGACAGAGGTTAAGGCCCTGGGGA	3415
QY	54	-----	54

Db	3420	GACGCTCGCACACAGAGGGGCGCCCTTAATTCATCATGCTTAACGCTTAACCTCGCCCTGACAGC	3419
QY	56	aCySePheProAspleuGlnHisGlyTyrLeuValAlaTyrLeuValLeuAspTyrThrSe	76
Db	3480	CTGCTTCCCGACACTTGACAGCAGGTTATCTGTGGCTGGTTGGTGCTGGACTACACAG	3539
QY	76	rAsPheLeuTyrIleuLeuAspMetValValArgPheHisThr-----	90
Db	3540	TGACTCGCTAATCACTACAGCATGATGGTGGCTTCCACAC-AGTGCATGGGCTTCTA	3598
QY	90	-----	90
Db	3599	GGATGACCCCTTGTCCCACTTCCCTTCTTAAGAATAGCCACTTAAGAACTAACAGAA	3658
QY	90	-----	90
Db	3659	AGGACACCCACCGTGGTAGCACTTGGCGCTTATGCTGACATCCAGTGTCT	3718
QY	90	-----	90
Db	3719	CACCCCGAAGACCGGAGAGAGATTATGCTGGCTCCACTGTGCTTACAGAGTCTC	3778
QY	90	-----	90
Db	3779	CCTGGCTGCCCTTGGGACGCTCATGCTGAGCCCAAGCTTGACTAGCAGAGGTCCGCTTCC	3838
QY	91	-----glyPheLeuGlnGlyIleuValValAspIysGlyAr	104
Db	3839	TACCGGCTCCCTCTCCCAAGATTCTTGAAACAGGGATCTGTGGTGGACAAAGGTAG	3898
QY	104	gIleSerSerArgTyrValArgThrTyrSerPhePheLeuAspLeuAserIleuMetPr	124
Db	3899	GATTCAGAGTCGCTACAGCTTGACCTGAGATTCTTGTGACCTGGCTTCCCTGATGCC	3958
QY	124	oThrAspValValTyrValArpleuGlyProHisThrProThrIleuArgLeuAsnArgPh	144
Db	3959	CACAGATGTGTCTACGTGCGGCTGGGCGGACACACCACTTGAGGCTGAACCCGCTT	4018
QY	144	eLeuArgAlaProArgLeuPheGlnAlaPheAspArgThrGlnThrArgThrAlaTyrPr	164
Db	4019	TCTCCGCGGCGCCCGGCTTTCAGAGGCTTCGACCGCACAGAGCCCGCACAGCTTACC	4078
QY	164	oAsnAlaPheArgIleAlaIysIleuMetLeuTyrIlePheValValIleHisTyrPAsnSe	184
Db	4079	AAATGCCCTTCGCAATGCCAAGCTGATGCTTTCATTTTGTGTCATCCATTGGAACAG	4138
QY	184	rCyLeuTyrPheAlaIleuSerArgTyrIleuGlyPheGlyArgAspAlaTyrValTyrPr	204
Db	4139	CTGCTAATCTTGGCCCTATCCCGGTAACCTGGGCTTCGGGCGTGAACCATGGGTAACC	4198
QY	204	oAspProAlaGlnProGlyPheGlnArgLeuArgArgGlnTyrLeuTyrSerPheTyrPh	224
Db	4199	GAGACCCCGGACCGCTTGTAAGCGCCCTCGGCGGCGCAGTACTCTATAGCTTTACTT	4258
QY	224	eSerThrLeuIleuThrThrValGlyAspThrProProProAlaArgGlnGlnIuTyr	244
Db	4259	CTCCACGCTGATCACTACACTGAACACTGCAGATGCGGCTTTCTACCCAAATCAATGC	4318
QY	244	rIleuPheMetValGlyAspPheLeuAlaValMetGlyPheAlaThrIleMetGlySe	264
Db	4319	CCCTCTCATAGTGGGAGACTCTCTGTGGCCGTCATGGGTTTGGCACCACTCATGGGTAG	4378
QY	264	rMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaAlaPheTyrProAspHisAl	284
Db	4379	CATGAGCTCTGTATCTTACACACTGAACACTGCAGATGCGGCTTTCTACCCAAATCAATGC	4438
QY	284	AlaValIysIysTyrMetIysLeuGlnHisValIaAsnArgIysLeuGlnArgArgValI1	304
Db	4439	ACTGGTGAAGAAAGTATCATGAAGCTGCAGACACGTCAACCCGAACTGGAGCGGAGTTAT	4498
QY	304	eAspTyr-----	306
Db	4499	TGACTGTGAGAGGCGGGGTTCACAGCAGACAGAGACCAAGTGTAGTGTATGAAACT	4558





Db 895 ACTGCTATATCGACACTCATCTATGCGCTCGCCACAGCGCTTCTAGAACAGGGGCTC 954  
 QY 98 LeuValValAspLysGlyArgIleSerSerArgTyrValArgThrTrpSerPhePheLeu 117  
 Db 995 TTGGTCAAGATCCCAAGAAATTTGGAGACCACTATATTCACACTTTCAGAGTTCAAAATTG 1014  
 QY 118 AspLeuAlaSerLeuMetProThrAspValValTyrValArgLeuGlyProHisThrPro 137  
 Db 1015 GATGGGCTTCTATATCCCACTGACCTATCTATTTTCTGCTGGGTATCCACAGCCCT 1074  
 QY 138 ThrLeuArgLeuAsnArgPheLeuArgAlaProArgLeuPheGluAlaPheAspArgThr 157  
 Db 1075 GAGGTACCGTTACCGTCTATATTAACCTTGGCCGATGTTGACTTCTTGAACCGCACT 1134  
 QY 158 GluThrArgThrAlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePhe 177  
 Db 1135 GAGACACGACACCACTACCCCAACATCTTCCGATCAGCAATCGTCTCTTACATCTTG 1194  
 QY 178 ValValIleHisTrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrIleuGlyPheGly 197  
 Db 1195 GTCATCATCTCCTGGAATGCTGTGATTTATTTATTTATTTTAAAGCCATTTGGCTTTGGA 1254  
 QY 198 ArgAspAlaTrpValTyrProAspProAlaGlnProGlyPheGluArgLeuArgGln 217  
 Db 1255 GTTGAACCTGGGTTTACCCCAACATTACTGACCCGTGAATATGGCTACCTGGCTGAGAG 1314  
 QY 218 TyrLeuTyrSerPheTyrPheSerThrIleuIleLeuThrValGlyAspThrProPro 237  
 Db 1315 TACATTTACTGCTTACTTACTGCTCACACTGACCCCTCACACCATTTGAGAGACACCC 1374  
 QY 238 ProAlaArgGluGlnGluTyrLeuPheMetValGlyAspPheLeuValAlaValMetGly 257  
 Db 1375 CTTGTAAGGATGAGAGAGTACTTATTTGTCATCTTGTGATCTTGTGTTGTTGTTCTCATC 1434  
 QY 258 PheAlaThrIleMetGlySerMetSerValIleTyrAsnMetAsnThrAlaAspAla 277  
 Db 1435 TTGGCACACTTGTGGGAATGTGGGCTCATGATCTCCAAACATGATGATCCACAGAGCA 1494  
 QY 278 AlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeuGlnHisValAsnArg 297  
 Db 1495 GAGTTCCAGGCCAAGATTGATGCTGTCAAAACATCATCATGCTCCGAAAGGCTGACGAAA 1554  
 QY 298 LysLeuGluArgArgValIleAspTrpTyrGlnHisLeuGlnIleAsnLysLysMetThr 317  
 Db 1555 GACATGGAGGCCAAGGCTATCAAAATGTTGACTTACTTGTGACCAATATGAGAGACAGTA 1614  
 QY 318 AsnGluValAlaIleLeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSer 337  
 Db 1615 GATGAACGAGAAAGTCTCTCAAGAACCTGCCAGCAAGGCTCAGGGCTGAGATGACATTAAT 1674  
 QY 338 ValHisLeuSerThrLeuSerArgValGlnIlePheGlnAsnGlyAlaSerLeuLeu 357  
 Db 1675 GTTCACTGTCTCACTGTGAAGAAAGTCCCATATTCAGAGATGTGTCAACCTGGCCCTACG 1734  
 QY 358 GluGluLeuValLeuLysLeuGlnProGlnThrTyrSerProGlyTyrValCysArg 377  
 Db 1735 GTGGAACTGTGACTGAAAGCTTGTCTCTCAGGCTTGTAGTCCCTGGAGATATATTTGCCCT 1794  
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 QY 398 AspAspGlyIleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGlnIleSer 417  
 Db 1855 GATGATGGGTGACTCAGATGCTCTGCTCAGCTGAGGAGCTGCTTGTGTGATGATTAAT 1914  
 QY 418 IleIleAsnIleLysGlyAsnMetSerGlyAsnArgTyrThrAlaAsnIleLysSerLeu 437  
 Db 1915 ATCTCTTAATTAAGGCTTACCAAAATGGGCAATGCAGTACTGCTTAATTCCTGACCTCG 1974  
 QY 438 GlyTyrSerAspLeuPheCysLeuSerLysGluAspLeuArgGluValLeuSerGlyTyr 457  
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QY 458 ProGlnAlaGlnThrIleMetGluGlnLysGlyArgGlnIleLeuLeuLysMetAsnLys 477  
 Db 2035 CCTGATGCCAAGAACCTGTGAGGAGACGGGTAGGAGATCTCTATGAAGATGGCTCTA 2094  
 QY 478 LeuAspValAsnAlaGluAlaAla-----GluIleAlaLeuGlnGluAlaThrGlnSer 495  
 Db 2095 CTGATGAGATGAAAGTGGCGACCTAGTATGAGATGATGATTTCCAGAG----- 2142  
 QY 496 ArgLeuArgGlyLeuAspGlnGlnLeuAspAspLeuGlnThrLysPheAlaArgLeuLeu 515  
 Db 2143 AAGCTGAACAGTTGGAGAACAAACATGATACCTGTACACTCGCTTGGCCCGCTGCTG 2202  
 QY 516 AlaGluLeuGlnSerSerAlaLeuLysIleAlaTyrArgIleGluArgLeuGlnTrpGln 535  
 Db 2203 GCTGATGACACTGGGGCCGACGAGAACTCAAGCAACGATACAGTGTCTAGAGACCAAG 2262  
 QY 536 ThrArgGluTrpProMetProGluAspLeuAlaGluAlaAspAspGluGlyGluPro 554  
 Db 2263 ATGAACACGAACCATGAGAGATGATATCTATCTATGATGGGATTAACACTCTGAGCCA 2319  
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 US-10-087-217-1  
 ; Sequence 1, Application US/10087217  
 ; Publication No. US20030100059A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aptus Genomics, Inc.  
 ; APPLICANT: YAO, Yong  
 ; APPLICANT: CAO, Liang  
 ; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Receptors  
 ; FILE REFERENCE: 53735-5004-US  
 ; CURRENT APPLICATION NUMBER: US/10/087,217  
 ; PRIOR FILING DATE: 2002-03-04  
 ; PRIOR APPLICATION NUMBER: 60/330,663  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1995  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1992)  
 ; OTHER INFORMATION:  
 ; US-10-087-217-1  
 Alignment Scores:  
 Pred. No.: 1,956-175 Length: 1995  
 Score: 1558.00 Matches: 292  
 Percent Similarity: 73.84% Conservative: 106  
 Best Local Similarity: 54.1% Mismatches: 135  
 Query Match: 52.12% Indels: 6  
 Gaps: 2  
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 QY 18 SerLysAlaArgLysLeuLeuProValLeuAspProSerGlyAspTyrTyrTrpTrp 37  
 Db 376 ACCAAAGAAATTGGAATGTTGTTTGGACCAAGCCGAGACTGTATTAACCTTGG 435  
 QY 38 LeuAsnThrMetValPheProValMetTyrAsnLeuIleIleLeuValCysArgAlaCys 57  
 Db 436 TTGTTTTCATTTGATGCTGCTGTTCTTCAACTGTGCTGCTGTGTGTGCTGACGAGCTGC 495  
 QY 58 PheProAspLeuGlnHisGlyTyrLeuValAlaTrpLeuValLeuAspTyrThrSerAsp 77  
 Db 496 TTCAGAGACTTACAGAGAACTATTTTGTGTATGCTGTGCTGTGACTTCTAGAC 555  
 QY 78 LeuLeuTyrLeuLeuAspMetValValArgPheHisThrGlyPheLeuGlnGlnGlyIle 97  
 Db 556 ACTGCTATATATGACGACCTCATCATCTCGGCTGGCAGACAGGCTTCTTAAACAGGGGCTC 615

QY	98	LeuValValAspIysrIysArgIleSerSerArgTyrValArgThrTyrSerPhePheLeu	117	QY	438	ProGlnAlaGlnThrIleMetGlnGluIysGlyArgGluIleLeuLeuIysMetAsnIys	477
Db	616	TTGGTCAAAGATCCCAAGAAATTGCGAGACACTATATACACTTTGGACGTTCAAATTG	675	Db	1696	CCTGATGCCAAGACAGAGCTCTGGAGGAACGGGGTATGGAGATCCTGATGAAGGAAGTCTA	1755
QY	118	AspLeuAlaSerLeuMetCProThrAspValValTyrValArgLeuGlyProHisThrPro	137	QY	478	LeuAspValAlaAspAlaGluIaIaA-----GluIleAlaLeuGlnGlnIaIaThrGlnSer	495
Db	676	GATGTGGCTTCATCATCTCCACTGACCTTATCTATTGTCGTGGGATTCACAGCCCT	735	Db	1756	CTGGATGAGATGAAAGTGGACGTAGTATGATGGAGTAAAGTATGACAGAG-----	1803
QY	138	ThrIleuArgLeuAsnArgPheLeuArgAlaProArgLeuPheGluIaIaPheAspArgThr	157	QY	496	ArgLeuArgGlyLeuAspGlnGlnLeuAspAspLeuGlnThrIysPheAlaArgLeuLeu	515
Db	736	GAGGTACGCTCAACCGCTATTAACACTTGGCCCGATGTTGAGTTCTTTACCGCACT	795	Db	1804	AAAGCTGAACAGTTGGAGCAACAACATGATACCTTGTAACCTCGCTTGGCCCGCTGCTG	1866
QY	158	GlnThrArgThrIaIaTyrProAsnAlaPheArgIleAlaIaIaLeuMetLeuTyrIlePhe	177	QY	516	AlaGlnLeuGlnSerSerAlaLeuIysIleAlaTyrArgIleGluArgLeuGlnTyrGln	535
Db	796	GAGACAGCACCGACTACCCCAACATCTTCGATGATAGCAACATCGGTCTTTACACTCTTG	855	Db	1864	GCTGAGTACACTGGGGCCCGACAGAGAAGCTCAAGCAACCATCACAGTCTAGAGCACCAAG	1923
QY	178	ValValIleHisTyrPheAsnSerCysLeuTyrPheAlaLeuSerArgTyrIleuGlyPheGly	197	QY	536	ThrArgGlnTyrProMetProGlnAspLeuIaIaGluIaIaAspAspGlnGlyGluPro	554
Db	856	GTCATGATCCACAGGAGATGCTGTATTATTATATATATATTTCTAAAGCTCACTGGCTCTTCTCA	915	Db	1924	ATGAAACCAAGACCATGAGATATATATCTATATGATGGGATAAACATCTCTGAGCA	1980





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OM protein - protein search, using SW model

Run on: September 11, 2004, 00:41:10 ; Search time 450 Seconds  
(without alignments)  
409.770 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDTKVKTTSSPPAPSKA.....EGTSKDEGRASQEGPPPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/2/pubpaa/US00\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2989	100.0	575	9	US-09-735-932-2
2	2989	100.0	575	9	US-09-927-267-1
3	2989	100.0	575	14	US-10-207-951-2
4	2984	99.8	575	10	US-09-842-758-30
5	2984	99.8	575	12	US-10-174-333-30
6	2984	99.8	575	16	US-10-311-624-1
7	2957.5	98.9	578	10	US-09-842-758-28
8	2957.5	98.9	578	12	US-10-174-333-28
9	2811	94.0	575	9	US-09-735-932-4
10	2811	94.0	575	9	US-09-927-267-16
11	2811	94.0	575	10	US-09-842-758-74
12	2811	94.0	575	12	US-10-174-333-74
13	2394	80.1	1704	14	US-10-207-951-4
14	1568	52.5	663	14	US-10-029-677-16
15	1565	52.4	664	14	US-10-295-573-5

16	1562	52.3	664	9	US-09-735-927-4	Sequence 4, Appli
17	1562	52.3	732	10	US-09-842-758-73	Sequence 73, Appl
18	1562	52.3	732	12	US-10-174-333-73	Sequence 73, Appl
19	1562	52.3	732	14	US-10-029-677-15	Sequence 15, Appl
20	1558	52.1	664	14	US-10-029-677-18	Sequence 18, Appl
21	1558	52.1	664	14	US-10-087-217-2	Sequence 2, Appli
22	1558	52.0	664	14	US-10-295-573-8	Sequence 8, Appli
23	1554	52.0	634	14	US-10-295-573-7	Sequence 7, Appli
24	1554	52.0	664	14	US-10-087-217-6	Sequence 6, Appli
25	1554	52.0	664	14	US-10-295-573-6	Sequence 6, Appli
26	1549.5	51.8	694	10	US-09-842-758-75	Sequence 75, Appl
27	1549.5	51.8	694	12	US-10-174-333-75	Sequence 75, Appl
28	1549.5	51.8	694	12	US-09-855-828-14	Sequence 14, Appl
29	1549.5	51.8	694	14	US-10-345-680-26	Sequence 26, Appl
30	1549	51.8	664	14	US-10-087-217-4	Sequence 4, Appli
31	1547	51.8	664	14	US-10-029-677-17	Sequence 17, Appl
32	1545	51.7	664	14	US-10-087-217-8	Sequence 8, Appli
33	1538.5	51.5	690	12	US-09-855-828-15	Sequence 15, Appl
34	1535	51.4	664	9	US-09-735-927-2	Sequence 2, Appli
35	1535	51.4	664	13	US-10-034-843-2	Sequence 2, Appli
36	1535	51.4	664	14	US-10-168-651-7	Sequence 7, Appli
37	1535	51.4	664	14	US-10-114-153-18	Sequence 18, Appl
38	1532	51.3	664	14	US-10-029-677-24	Sequence 24, Appl
39	1529	51.2	664	14	US-10-029-677-2	Sequence 2, Appli
40	1208	40.4	239	15	US-10-189-507-10	Sequence 10, Appl
41	1196	40.0	239	15	US-10-189-507-6	Sequence 6, Appli
42	779	26.1	239	15	US-10-189-507-5	Sequence 5, Appli
43	773	25.9	239	15	US-10-189-507-9	Sequence 9, Appli
44	769	25.7	239	15	US-10-189-507-12	Sequence 12, Appl
45	655	21.9	809	12	US-09-855-828-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-735-932-2  
; Sequence 2, Application US/09735932  
; Patent No. US20020037548A1  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,  
; FILE REFERENCE: C1000663  
; CURRENT APPLICATION NUMBER: US/09/735, 932  
; CURRENT FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Human  
US-09-735-932-2

Query Match 100.0%; Score 2989; DB 9; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2.8e-266;  
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSQDTKVKTTSSPPAPSKAKLLPVLDPGSDYVWMLNTWVPMNLILVCRACPD	60
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QY	61	LQHYIVAMVLVDYTSLLVLLDMVVFPHGFLFQGLIVVDKGRISRYVTSFFDLA	120
DB	61	LQHYIVAMVLVDYTSLLVLLDMVVFPHGFLFQGLIVVDKGRISRYVTSFFDLA	120
QY	121	SIMPTDVVYVRLGHTPTLRLNRLRAPRLPEADRTETRYVNAFRIAKMLYIFVI	180
DB	121	SIMPTDVVYVRLGHTPTLRLNRLRAPRLPEADRTETRYVNAFRIAKMLYIFVI	180
QY	181	HMNSCLVFSRYIGFGRDAVYDPDPAQPFERILROYLVSFFSTLITVGDTPPAR	240
DB	181	HMNSCLVFSRYIGFGRDAVYDPDPAQPFERILROYLVSFFSTLITVGDTPPAR	240

Db 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRQYLSGFYSTLLITTVGDTPPAR 240  
QY 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300  
Db 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300  
QY 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHTLSRVQIFONCEASLLEEL 360  
Db 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHTLSRVQIFONCEASLLEEL 360  
QY 361 VLKLPQPTSPGFEYVCRKGDIGQEMYYIIRREGQLAVVADGITOYAVLAGYFGEISITN 420  
Db 361 VLKLPQPTSPGFEYVCRKGDIGQEMYYIIRREGQLAVVADGITOYAVLAGYFGEISITN 420  
QY 421 IKGNMGNRRNTANKISLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480  
Db 421 IKGNMGNRRNTANKISLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480  
QY 481 NAAAEIALQEATSRRLKGLDQDLDTQKFAFLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAAEIALQEATSRRLKGLDQDLDTQKFAFLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGE 575  
Db 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGE 575

## RESULT 2

US-09-927-267-1  
; Sequence 1, Application US/09927267  
; Publication No. US20020182691A1  
; GENERAL INFORMATION:  
; APPLICANT: Creech, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICGem, Inc.  
; TITLE OF INVENTION: CNG2B: A No. US20020182691A1 Human Cyclic Nucleotide-Gated Ion  
; TITLE OF INVENTION: Channel  
; FILE REFERENCE: 018512-006510US  
; CURRENT APPLICATION NUMBER: US/09/927,267  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/226,253  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)  
US-09-927-267-1

Query Match 100.0%; Score 2989; DB 9; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2,8e-266;  
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQDTKXVTTSSPPAPSKARKLIPVLDPSGDYYWYNNNTADAAFYDPHALVKKYMKLQHNKRL 60  
Db 1 MSQDTKXVTTSSPPAPSKARKLIPVLDPSGDYYWYNNNTADAAFYDPHALVKKYMKLQHNKRL 60  
QY 61 LOHGLVAMLVLDYSDLLYLIDMWVVRFTGFLREGILVVDKGRISSRVRRWSSFFLDA 120  
Db 61 LOHGLVAMLVLDYSDLLYLIDMWVVRFTGFLREGILVVDKGRISSRVRRWSSFFLDA 120  
QY 121 SLMPDYYVYRGLPPTPLRLNRFARAPLFEAFRTETRTAYPAAPRIAKMLIYFYVI 180  
Db 121 SLMPDYYVYRGLPPTPLRLNRFARAPLFEAFRTETRTAYPAAPRIAKMLIYFYVI 180  
QY 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRQYLSGFYSTLLITTVGDTPPAR 240  
Db 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRQYLSGFYSTLLITTVGDTPPAR 240  
QY 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300

Db 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300  
QY 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHTLSRVQIFONCEASLLEEL 360  
Db 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHTLSRVQIFONCEASLLEEL 360  
QY 361 VLKLPQPTSPGFEYVCRKGDIGQEMYYIIRREGQLAVVADGITOYAVLAGYFGEISITN 420  
Db 361 VLKLPQPTSPGFEYVCRKGDIGQEMYYIIRREGQLAVVADGITOYAVLAGYFGEISITN 420  
QY 421 IKGNMGNRRNTANKISLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480  
Db 421 IKGNMGNRRNTANKISLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480  
QY 481 NAAAEIALQEATSRRLKGLDQDLDTQKFAFLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAAEIALQEATSRRLKGLDQDLDTQKFAFLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGE 575  
Db 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGE 575

## RESULT 3

US-10-207-951-2  
; Sequence 2, Application US/10207951  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: Karl GUEGLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: C1000663CON  
; CURRENT APPLICATION NUMBER: US/10/207,951  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-951-2

Query Match 100.0%; Score 2989; DB 14; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2,8e-266;  
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQDTKXVTTSSPPAPSKARKLIPVLDPSGDYYWYNNNTADAAFYDPHALVKKYMKLQHNKRL 60  
Db 1 MSQDTKXVTTSSPPAPSKARKLIPVLDPSGDYYWYNNNTADAAFYDPHALVKKYMKLQHNKRL 60  
QY 61 LOHGLVAMLVLDYSDLLYLIDMWVVRFTGFLREGILVVDKGRISSRVRRWSSFFLDA 120  
Db 61 LOHGLVAMLVLDYSDLLYLIDMWVVRFTGFLREGILVVDKGRISSRVRRWSSFFLDA 120  
QY 121 SLMPDYYVYRGLPPTPLRLNRFARAPLFEAFRTETRTAYPAAPRIAKMLIYFYVI 180  
Db 121 SLMPDYYVYRGLPPTPLRLNRFARAPLFEAFRTETRTAYPAAPRIAKMLIYFYVI 180  
QY 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRQYLSGFYSTLLITTVGDTPPAR 240  
Db 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRQYLSGFYSTLLITTVGDTPPAR 240  
QY 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300  
Db 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVYNNNTADAAFYDPHALVKKYMKLQHNKRL 300  
QY 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHTLSRVQIFONCEASLLEEL 360

Db 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHLSTLSVQIFONCEASLLEBL 360  
QY 361 VLKLPQPTYSPEGYCRKGDIGQEMYYIIRREGQLAVADGITYAVLGAIFYGEISITIN 420  
Db 361 VLKLPQPTYSPEGYCRKGDIGQEMYYIIRREGQLAVADGITYAVLGAIFYGEISITIN 420  
QY 421 IKGNNSGNRRRTANIKSLGYSDLPCLSKEDLREVLSYEPQAQTIMEEKREIILLKXNKLDV 480  
Db 421 IKGNNSGNRRRTANIKSLGYSDLPCLSKEDLREVLSYEPQAQTIMEEKREIILLKXNKLDV 480  
QY 481 NAAAEIALQEAATESRLRGDLQDLDTQKFAILLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAAEIALQEAATESRLRGDLQDLDTQKFAILLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575  
Db 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575

## RESULT 4

US-09-842-758-30  
; Sequence 30, Application US/09842758  
; Publication No. US20030083244A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Shinkels, Richard A.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Zernhusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tchiernev, Velizar T.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patuturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gangoli, Esna A.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Rastelli, Luca  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Grose, William M.  
; APPLICANT: Edward, Szekeres S.  
; APPLICANT: Alsobrook II, John P.  
; TITLE OF INVENTION: No. US20030083244a1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 1596-783  
; CURRENT APPLICATION NUMBER: US/09/842,758  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/200,158  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/200,613  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,780  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/201,006  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,007  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,236  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,238  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,186  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 60/201,474  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/201,508  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/220,591  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: 60/232,678

; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/263,217  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-842-758-30

Query Match 99.8%; Score 2984; DB 10; Length 575;  
Best Local Similarity 99.8%; Pred No. 8.2e-266;  
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQDTKVTSSPPAPSKARKLPVLDPSGDYYMMINTWFPVYMLIILVCACFPD 60  
Db 1 MSQDTKVTSSPPAPSKARKLPVLDPSGDYYMMINTWFPVYMLIILVCACFPD 60  
QY 61 LQHGIVAMVLVDYSDLLIYLDKYYRHTGFLBEGIIVDKGRISRYRTWSTFLLDA 120  
Db 61 LQHGIVAMVLVDYSDLLIYLDKYYRHTGFLBEGIIVDKGRISRYRTWSTFLLDA 120  
QY 121 SLMPDYYVYVLRGPTPTLRNLRLAPRLFEAPRTEPTTRAYPNAPRIKIMLYIPLYI 180  
Db 121 SLMPDYYVYVLRGPTPTLRNLRLAPRLFEAPRTEPTTRAYPNAPRIKIMLYIPLYI 180  
QY 181 HWSCLYPALSRYYJGFGSDAWVPDPAQPGFERLRQYLYSFFSTLITLVGDTPPPAR 240  
Db 181 HWSCLYPALSRYYJGFGSDAWVPDPAQPGFERLRQYLYSFFSTLITLVGDTPPPAR 240  
QY 241 EEEYLFMGDPLLAVMGATITMGSSVITYMMNTDAAPYPHALVKKYMKI QHNRKIE 300  
Db 241 EEEYLFMGDPLLAVMGATITMGSSVITYMMNTDAAPYPHALVKKYMKI QHNRKIE 300  
QY 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHLSTLSVQIFONCEASLLEBL 360  
Db 301 RRVIDWYQHLQINKKMTNEVALIQLPERLRAEVAVSHLSTLSVQIFONCEASLLEBL 360  
QY 361 VLKLPQPTYSPEGYCRKGDIGQEMYYIIRREGQLAVADGITYAVLGAIFYGEISITIN 420  
Db 361 VLKLPQPTYSPEGYCRKGDIGQEMYYIIRREGQLAVADGITYAVLGAIFYGEISITIN 420  
QY 421 IKGNNSGNRRRTANIKSLGYSDLPCLSKEDLREVLSYEPQAQTIMEEKREIILLKXNKLDV 480  
Db 421 IKGNNSGNRRRTANIKSLGYSDLPCLSKEDLREVLSYEPQAQTIMEEKREIILLKXNKLDV 480  
QY 481 NAAAEIALQEAATESRLRGDLQDLDTQKFAILLAELESSALKIAYRIERLEWQTRMP 540  
Db 481 NAAAEIALQEAATESRLRGDLQDLDTQKFAILLAELESSALKIAYRIERLEWQTRMP 540  
QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575  
Db 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575

## RESULT 5

US-10-174-333-30  
; Sequence 30, Application US/10174333  
; Publication No. US20040029220A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Zernhusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tchiernev, Velizar T.  
; APPLICANT: Padigaru, Muralidhara

```
APPLICANT: Paturajan, Weera
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangoli, Esna A.
APPLICANT: Sathson, Glenda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Taupier, Raymond J.
APPLICANT: Grosse, William M.
APPLICANT: Szekeres, Edward S.
APPLICANT: Alsobrook, John P.
APPLICANT: Anderson, David W.
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Li, Li
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-783 CIP1
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/193,664
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,063
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,066
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,067
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,068
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,069
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,070
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,510
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/219,855
PRIOR FILING DATE: 2000-07-21
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 186
SOFTWARE: CursSeqList version 0.1
SEQ ID NO 30
LENGTH: 575
TYPE: PRT
ORGANISM: Homo sapiens
US-10-174-333-30

Query Match          99.8%; Score 2984; DB 12; Length 575;
Best Local Similarity 99.8%; Pred. No. 8.2e-266;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQDTKVTSSPPAPSKARKLLPVLDPSGDYYWMTNMFPMYNLIIVCRACFPD 60
DB 1 MSQDTKVTSSPPAPSKARKLLPVLDPSGDYYWMTNMFPMYNLIIVCRACFPD 60
QY 61 LQHGIVAMVLVDYSDLLYLDMVVRFTGTGLEGGILVVDKGRISRYRTWMSFFDLA 120
DB 61 LQHGIVAMVLVDYSDLLYLDMVVRFTGTGLEGGILVVDKGRISRYRTWMSFFDLA 120
QY 121 SLMPDVVVYVRLGPHPTPLRLNRLRAPRLFEAFPRTRTRAYPAFAIAKMLYIFVYI 180
DB 121 SLMPDVVVYVRLGPHPTPLRLNRLRAPRLFEAFPRTRTRAYPAFAIAKMLYIFVYI 180
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DB 181 HNSCLTYFALSRYLGFGRDAMVYPPAOPGFERLRQYLYSFYFTLLITVGDTPPAR 240
QY 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYDPHALVKKYMKLOHVNKLE 300
DB 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYDPHALVKKYMKLOHVNKLE 300
QY 301 RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEEL 360
DB 301 RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEEL 360
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DB 301 RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEEL 360
QY 361 VLKLOPOTYSPEGEYCCRGDGGEMTIRREGOLAVVADGGITTOYAVLAGAGYFGISITIN 420
DB 361 VLKLOPOTYSPEGEYCCRGDGGEMTIRREGOLAVVADGGITTOYAVLAGAGYFGISITIN 420
QY 421 IKGNWGNRRRTANIKSLGYSDLPCLSKEDLREVLEYEQAOITIBEKREITILKMKKLDV 480
DB 421 IKGNWGNRRRTANIKSLGYSDLPCLSKEDLREVLEYEQAOITIBEKREITILKMKKLDV 480
QY 481 NAAEAIALQATSRRLNGLDQOQDDLOTKPARLLAEISSALKIAYRIEIEWOTRWP 540
DB 481 NAAEAIALQATSRRLNGLDQOQDDLOTKPARLLAEISSALKIAYRIEIEWOTRWP 540
QY 541 MPEDLAENDDEGEPEEGTSKDEGRASGEGPPE 575
DB 541 MPEDLAENDDEGEPEEGTSKDEGRASGEGPPE 575

RESULT 6
US-10-311-624-1
Sequence 1, Application US/10311624
Publication No. US20040127683A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: RAUMANN, Brigitte E.
APPLICANT: Sanjanwala, Madhu S.
APPLICANT: TRIBOUTY, Catherine K.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: SI-0141 PCT
CURRENT FILING DATE: US/10/311,624
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/215,391
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 575
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6703242CD1
US-10-311-624-1

Query Match          99.8%; Score 2984; DB 16; Length 575;
Best Local Similarity 99.8%; Pred. No. 8.2e-266;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MSQDTKVTSSPPAPSKARKLLPVLDPSGDYYWMTNMFPMYNLIIVCRACFPD 60
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DB 61 LQHGIVAMVLVDYSDLLYLDMVVRFTGTGLEGGILVVDKGRISRYRTWMSFFDLA 120
QY 121 SLMPDVVVYVRLGPHPTPLRLNRLRAPRLFEAFPRTRTRAYPAFAIAKMLYIFVYI 180
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DB 181 HNSCLTYFALSRYLGFGRDAMVYPPAOPGFERLRQYLYSFYFTLLITVGDTPPAR 240
QY 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYDPHALVKKYMKLOHVNKLE 300
DB 241 EEEYLFMWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYDPHALVKKYMKLOHVNKLE 300
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DB 301 RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASILEEL 360
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-842-758-28  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
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; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
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; LENGTH: 578  
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; ORGANISM: Homo sapiens  
RESULT 7  
US-09-842-758-28  
; Sequence 28, Application US/09842758  
; Publication No. US20030083244A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldo, Ferenc L.  
; APPLICANT: Zethusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tchernen, Velizar T.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gangoli, Esna A.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Rastrelli, Luca  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Grose, William M.  
; APPLICANT: Edward, Szekeres S.  
; APPLICANT: Alsobrook II, John P.  
; TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-783  
; CURRENT APPLICATION NUMBER: US/09/842,758  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/200,158  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/200,613  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,780  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/201,006  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,007  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,236  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,228  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/201,186  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 60/201,474  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/201,508  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 60/220,591  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: 60/232,678  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/263,217

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; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; NUMBER OF SEQ ID NOS: 113  
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; SEQ ID NO 28  
; LENGTH: 578  
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; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
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; SEQ ID NO 28  
; LENGTH: 578  
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; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 119 LASLMPDVVYVRLGPHPTTLRLNRFAPRLFEAFDRTETRTAYPNAFRIAKMLYIFV 178  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 121 LASLMPDVVYVRLGPHPTTLRLNRFAPRLFEAFDRTETRTAYPNAFRIAKMLYIFV 180  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 181 VIHNNSCLYFALSRIGFGRAMVYPPDAQGFPERLRQYLYSFFSTLITTVGDTTPP 240  
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; PRIOR APPLICATION NUMBER: 60/265,160  
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; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 239 ARSEYFLPMVDLFLAVVGFATTMGSSSVLYNMNTADAAFPDHALVKYMKLQHNK 298  
; PRIOR FILING DATE: 2001-01-22  
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; PRIOR FILING DATE: 2000-01-30  
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; SOFTWARE: Patencin Ver. 2.1  
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; LENGTH: 578  
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Db 241 ARSEYFLPMVDLFLAVVGFATTMGSSSVLYNMNTADAAFPDHALVKYMKLQHNK 300  
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; SOFTWARE: Patencin Ver. 2.1  
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; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 299 LERRVIDMYOHLQINKKNTNEVAILQHLPERLRAEVAVSHLSTLSRVQIFQNCBASLLE 358  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 301 LERRVIDMYOHLQINKKNTNEVAILQHLPERLRAEVAVSHLSTLSRVQIFQNCBASLLE 360  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 359 ELVILKQPYTSPEEYVCRKDDIQEWYIIREGQLAVVADGITOYAVLGAAGLYFGESII 418  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 361 ELVILKQPYTSPEEYVCRKDDIQEWYIIREGQLAVVADGITOYAVLGAAGLYFGESII 420  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 419 INIK-GNMSGNRKRNITKSLGSDLFCLSKEDLREVSEYPOAQTIMEKREIILLKXNK 477  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 421 INIK-GNMSGNRKRNITKSLGSDLFCLSKEDLREVSEYPOAQTIMEKREIILLKXNK 480  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 478 LDVNAEAEIALQEATERSRLRGDLDDLOQTKFARLLAELESSALKIAYRIERLEWQTR 537  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 481 LDVNAEAEIALQEATERSRLRGDLDDLOQTKFARLLAELESSALKIAYRIERLEWQTR 540  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
QY 538 EMPMEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
Db 541 EMPMEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 578  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 60/265,160  
; PRIOR FILING DATE: 2000-01-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
RESULT 8  
US-10-174-333-28  
; Sequence 28, Application US/10174333  
; Publication No. US20040029220A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A. M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldo, Ferenc L.  
; APPLICANT: Zethusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tchernen, Velizar T.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Paturajan, Meera  
; APPLICANT: Burgess, Catherine E.





QY 481 NAAEAELIAGQETTERLRIGDOODLQKFAILLAEISSAKIAYRIERLEWQREWP 540  
Db 481 NAAEAELIAGQETTERLRIGDOODLQKFAILLAEISSAKIAYRIERLEWQREWP 540  
QY 541 MPEDLAEADDEGEPEEGTSTKDEGRASQGEPPGE 575  
Db 541 MPEDMGADDEAEFEGTSTKDEGRASQGEPPGE 575

```

RESULT 10
US-09-927-267-16
Sequence 16, Application US/09927267
Publication No. US20020182691A1
GENERAL INFORMATION:
APPLICANT: Creech, Christopher D.
APPLICANT: Creech, Timothy J.
APPLICANT: ICogen, Inc.
TITLE OF INVENTION: CNG2: A No. US20020182691A1 Human Cyclic Nucleotide-Gated Ion
TITLE OF INVENTION: Channel1
FILE REFERENCE: 018512-006510US
CURRENT APPLICATION NUMBER: US/09/927,267
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/226,253
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 575
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: rat cyclic nucleotide gated cation channel CNGC2
US-09-927-267-16

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Query Match	94.0%	Score 2811;	DB 9;	Length 575;
Best Local Similarity	93.4%	Pred. No. 7.3e-250;		
Matches 537;	Conservative 16;	Mismatches 22;	Indels 0;	Gaps 0.

QY	MSODKRYKTTESPPAPSKARKLLEVVLDPSGDYYWMLNTWFPVWNLILVCRACFPD	60
Db	MSQDQKVATTESTPAPFTKARKMLFVLBPSGDYYWMLNTWFPIMYNLILVCRACFPD	60
QY	LOHGVLVAMVLVDYSDLLYLLDMVVRPHGTGLEGGILVYDKRISRYVYTWSEFLDLA	120
Db	LQHSVLVAMFVLVDYSDLLYLLDGVRRHGTGLEGGILVYDKMIASRYVYTWSEFLDLA	120
QY	SLMPTDVVYVRLGPHTPTLRLNRLFLAARLEFEAFRETRETCAVYNAFIAKMLYIYVVI	180
Db	SLVPTDAVAYVQGHPIPLRLNRLFLVRVRLLEADRDRETKRAYNARIRAKMLYIYVVI	180
QY	HMNSTLYALSRYYLGFGEADVAYYDDPAOPGGERLROYLSFYFSTLILTVGDTPPPAR	240
Db	HMNSTLYALSRYYLGFGEADVAYYDDPAOPGGERLRQVLSFYFSTLILTVGDTPLPDR	240
QY	EEEYLFPMVGDLLVWGFATIMSGMSSTIYMMNLADAAFPDHALYKKMKLQHVNRKLE	300
Db	EEBILFPMVGDLLVWGFATIMSGMSSTIYMMNLADAAFPDHALYKKMKKLHVNRKLE	300
QY	RRVIDWYQHLQINKKMTNEVALILQHLBERLRAEYAVSVHSTLSRVQIIPONCASLLEEL	360
Db	RRVIDWYQHLQINKKMTNEVALILQHLBERLRAEYAVSVHSTLSRVQIPONCASLLEEL	360
QY	VLKIQPOTYSBGEVYVCKRKGDIQCEMYIIRREGQLAVVADGITOYAVLGAELYGEISIN	420
Db	VLKIQPOTYSBGEVYVCKRKGDIGREMYIIRREGQLAVVADGVTQYAVLGAELYGEISIN	420
QY	IKGMSNRRSTANIKSLGYSDLPCLSEDLREVLSEYPAQOTIMEKGRFILLKXNKLDV	480
Db	IKGMSNRRSTANIKSLGYSDLPCLSEDLREVLSEYPAQOAVMEKGRFILLKXNKLDV	480
QY	NAEAAETALQEAATESRLRGDQOOLDQOTFARLLAELESASAKIYRERLEWQREWP	540
Db	NAEAAETALQEAATESRLRGDQOOLDQOTFARLLAELESASAKIYRERLEWQREWP	540

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QY      541 MPEEDLAADDEGEPEEGTSTKDEEGRASQEGPPGE 579
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Db      541 MPEEDMGEADDEAEPGEETSKDGEKGAGQAGPSGIE 579
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```

RESULT 11
US-09-842-758-74
; Sequence 74, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigara, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangoli, Esna A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grose, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsbrook II, John P
; TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-842-758-74

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RESULT 12  
US-10-174-333-74  
Sequence 74, Application US/10174333  
Publication No. US20040029220A1  
GENERAL INFORMATION:  
APPLICANT: Vermet, Corine A.M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Malynkar, Uriel M.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Szytek, Kimberly A.  
APPLICANT: Majumder, Kundu  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Padisaru, Muralidhara  
APPLICANT: Patutajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gangoli, Esna A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Restelli, Luca  
APPLICANT: Macdonough, John R.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Grose, William M.  
APPLICANT: Ssekeres, Edward S.  
APPLICANT: Alsobrook, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Li, Li  
APPLICANT: Zhong, Mei

QY	I	MSO	T	K	T	T	T	S	S	P	A	K	K	L	P	V	D	P	S	G	D	Y	Y	M	M	L	N	T	M	E	P	W	N	L	I	I	V	C	A	C	E	P	D	60												
Db	1	MSO	G	K	V	T	T	S	T	P	A	P	A	K	K	L	P	V	D	P	S	G	D	Y	Y	M	M	L	N	T	M	E	P	W	N	L	I	I	V	C	A	C	E	P	D	60										
QY	61	LQ	H	G	I	V	A	M	L	V	D	Y	S	D	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	120											
Db	61	LQ	H	G	I	V	A	M	L	V	D	Y	S	D	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	120											
QY	121	S	L	M	P	D	V	Y	V	L	G	P	H	T	P	L	T	L	N	R	F	L	A	R	L	F	E	A	P	O	R	T	E	R	T	A	Y	P	A	N	F	A	K	M	L	Y	F	V	Y	180						
Db	121	S	L	M	P	D	V	Y	V	L	G	P	H	T	P	L	T	L	N	R	F	L	A	R	L	F	E	A	P	O	R	T	E	R	T	A	Y	P	A	N	F	A	K	M	L	Y	F	V	Y	180						
QY	181	H	M	N	S	C	L	F	A	L	S	R	I	L	G	F	G	R	D	A	W	Y	P	D	P	A	O	G	F	E	R	L	R	O	Y	I	S	E	F	S	T	L	L	I	T	Y	G	D	T	P	P	A	R	240		
Db	181	H	M	N	S	C	L	F	A	L	S	R	I	L	G	F	G	R	D	A	W	Y	P	D	P	A	O	G	F	E	R	L	R	O	Y	I	S	E	F	S	T	L	L	I	T	Y	G	D	T	P	P	A	R	240		
QY	241	E	E	E	L	F	M	I	G	D	E	L	L	A	M	G	F	A	T	I	M	G	S	S	V	Y	N	N	N	T	D	A	A	E	Y	P	H	A	L	V	K	K	M	L	O	H	N	V	K	R	L	E	300			
Db	241	E	E	E	L	F	M	I	G	D	E	L	L	A	M	G	F	A	T	I	M	G	S	S	V	Y	N	N	N	T	D	A	A	E	Y	P	H	A	L	V	K	K	M	L	O	H	N	V	K	R	L	E	300			
QY	301	R	E	V	I	D	M	Y	O	H	L	I	N	K	K	O	T	N	E	V	A	L	L	O	H	L	P	E	R	L	A	R	A	V	A	S	V	A	L	S	T	S	R	O	I	F	O	N	C	A	S	L	L	E	L	360
Db	301	R	E	V	I	D	M	Y	O	H	L	I	N	K	K	O	T	N	E	V	A	L	L	O	H	L	P	E	R	L	A	R	A	V	A	S	V	A	L	S	T	S	R	O	I	F	O	N	C	A	S	L	L	E	L	360
QY	361	V	K	L	O	P	O	T	S	P	E	G	Y	O	R	K	D	I	G	O	E	M	T	I	R	E	G	O	L	A	V	A	D	D	G	I	O	Y	A	V	L	G	A	G	I	Y	E	G	E	I	S	I	N	420		
Db	361	V	K	L	O	P	O	T	S	P	E	G	Y	O	R	K	D	I	G	O	E	M	T	I	R	E	G	O	L	A	V	A	D	D	G	I	O	Y	A	V	L	G	A	G	I	Y	E	G	E	I	S	I	N	420		
QY	421	I	K	G	N	S	G	N	R	T	A	N	I	K	S	I	G	S	D	L	F	C	S	K	E	D	L	R	E	V	L	S	E	P	O	A	Q	T	M	E	R	K	E													

QY 541 MPEDLAEDDGEPEEGTSKDEGRASOEGPPGPE 575  
 Db 541 MPEDMGADDEAFEGEGTSKDEGRAGAGPSGIE 575

RESULT 13

US-10-207-951-4  
 ; Sequence 4, Application US/10207951  
 ; Publication No. US20030013156A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Karl GUEGLER et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS  
 ; FILE REFERENCE: CLO00663CON  
 ; CURRENT APPLICATION NUMBER: US/10/207,951  
 ; PRIOR FILING DATE: 2002-07-31  
 ; PRIOR APPLICATION NUMBER: 09/735,932  
 ; PRIOR FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 60/211,223  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1704  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-207-951-4

Query Match 80.1%; Score 2394; DB 14; Length 1704;  
 Best Local Similarity 37.1%; Pred. No. 1,1e-210;  
 Matches 567; Conservative 5; Mismatches 3; Indels 952; Gaps 9;

QY 1 MSODTKYKTESPPAPSKARKLPLVDPGSDYYMMNTMVPVYNTLILVCRACPD 60  
 Db 117 MSQCKKTTSTPAPKARKMLPLDPSGDYYMMNTMVPVYNTLILVCRACPD 176  
 QY 61 -LQHGVLVAMVLVDYSDLLVLDVYVFRHTGFLGQGLVVDKGRISRYRTWSFLLD 119  
 Db 177 QLQHGVLVAMVLVDYSDLLVLDVYVFRHTGFLGQGLVVDKGRISRYRTWSFLLD 236  
 QY 120 A----- 120  
 Db 237 ALQHYLVAMVLVDYSDLLVLDVYVFRHTGFLGQGLVVDKGRISRYRTWSFLLD 296  
 QY 121 -----SIMP 124  
 Db 297 LVAMFVLVDYSDLLVLDVYVFRHTGFLGQGLVVDKGRISRYRTWSFLLD 356  
 QY 125 TDVVYVRLGPHPTPLRLNRLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVI 180  
 Db 357 TDVVYVRLGPHPTPLRLNRLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVI 416  
 QY 181 ----- 180  
 Db 417 DYVLGPHPTPLRLNRLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVISLVPDAAY 476  
 QY 181 -----HMNSCLYF 188  
 Db 477 VOLGPHPTPLRLNRLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVIQHMNSCLYF 536  
 QY 189 ALSRYLGFGRDAWYPPDPAQGFGERLRRQYLYSFYSTLLITLTVGDTPPRPAR 240  
 Db 537 ALSRYLGFGRDAWYPPDPAQGFGERLRRQYLYSFYSTLLITLTVGDTPPRPARHNSCLYF 596  
 QY 241 ----- 240  
 Db 597 ALSRYLGFGRDAWYPPDPAQGFGERLRRQYLYSFYSTLLITLTVGDTPPRSHMNSCLYFA 656  
 QY 241 -----EEEYLFMV 248  
 Db 657 LSRYLGFGRDAWYPPDPAQGFGERLRRQYLYSFYSTLLITLTVGDTPLPDRQEEYLFMV 716

QY 249 GDFLLAVMGFATINGSMSVLYNNMTADAAFYPDHALVKYMKLQHVNRKLE----- 300  
 Db 717 GDFLLAVMGFATINGSMSVLYNNMTADAAFYPDHALVKYMKLQHVNRKLEEEYLFMV 776  
 QY 301 ----- 300  
 Db 777 GDFLLAVMGFATINGSMSVLYNNMTADAAFYPDHALVKYMKLQHVNLSEEEYLFMV 836  
 QY 301 ----- 300  
 Db 837 DFLAVMGFATINGSMSVLYNNMTADAAFYPDHALVKYMKLQHVNRKLEQRYVIDYQ 896  
 QY 301 ----- 300  
 Db 897 HLQINKKMSNEVALIQLHPLERLRAEVAVSVHLSTLSRVQIFQNCESASILEELRRYVIDYQ 956  
 QY 301 -----RRYVIDYQ 308  
 Db 957 HLQINKKMSNEVALIQLHPLERLRAEVAVSVHLSTLSRVQIFQNCESASILEELRRYVIDYQ 1016  
 QY 309 HLQINKKMSNEVALIQLHPLERLRAEVAVSVHLSTLSRVQIFQNCESASILEEL-VLKLQPO 367  
 Db 1017 HLQINKKMSNEVALIQLHPLERLRAEVAVSVHLSTLSRVQIFQNCESASILEELQVLKQPO 1076  
 QY 368 TYSPEYVCRKGDIGQEMYYIIRREGQLAVVADGDTQYAVLAGAGLYFGESITIN----- 420  
 Db 1077 TYSPEYVCRKGDIGQEMYYIIRREGQLAVVADGDTQYAVLAGAGLYFGESITINVLKQPO 1136  
 QY 421 ----- 420  
 Db 1137 TYSPEYVCRKGDIGEMYYIIRREGQLAVVADGDTQYAVLAGAGLYFGESITINVLKQPO 1196  
 QY 421 ----- 420  
 Db 1197 YSPGEYVCRKGDIGREMYIIRREGQLAVVADGDTQYAVLAGAGLYFGESITINQKNNSG 1256  
 QY 421 ----- 420  
 Db 1257 NRRNTNKSIGYSDLPCLSKEDLREVLSYEPQAOQMEKGRITLLKMKLDVSKNNSG 1316  
 QY 421 -----IKNNSGNRR 430  
 Db 1317 NRRNTNKSIGYSDLPCLSKEDLREVLSYEPQAOQMEKGRITLLKMKLDVSKNNSGNRR 1376  
 QY 431 TANIKSLGYSDLPCLSKEDLREVLSYEPQAOQMEKGRITLLKMKLDV-NAAEAETAL 489  
 Db 1377 TANIKSLGYSDLPCLSKEDLREVLSYEPQAOQMEKGRITLLKMKLDVQNAEAETAL 1436  
 QY 490 QEATESRLRGDQDLQDTKFAFLAELSSALKIYRIERLEWQREMP----- 540  
 Db 1437 QEATESRLRGDQDLQDTKFAFLAELSSALKIYRIERLEWQREMPNAAETAL 1496  
 QY 541 ----- 540  
 Db 1497 QEATESRLRGDQDLQDTKFAFLAELSSALKIYRIERLEWQREMPNAAETAL 1556  
 QY 541 -----MPEDLAEA 548  
 Db 1557 QEATESRLRGDQDLQDTKFAFLAELSSALKIYRIERLEWQREMPMPEDLAEA 1616  
 QY 549 DDEGEPEEGTSKDEGRASOEGPPGPE 575  
 Db 1617 DDEGEPEEGTSKDEGRASOEGPPGPE 1643

RESULT 14

US-10-029-677-16  
 ; Sequence 16, Application US/10029677  
 ; Publication No. US20030096249A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Westphal, Ryan S.  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Ramanathan, Chandra S.

APPLICANT: Mintier, Gabriel A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL  
FILE REFERENCE: D0187NP  
CURRENT APPLICATION NUMBER: US/10/029,677  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: US 60/257,865  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16  
LENGTH: 663  
TYPE: PRT  
ORGANISM: Bos taurus  
US-10-029-677-16

Query Match 52.5%; Score 1568; DB 14; Length 663;  
Best Local Similarity 54.2%; Pred. No. 3.8e-135;  
Matches 292; Conservative 108; Mismatches 133; Indels 6; Gaps 2;

QY 18 SKARKLIPVLDPSGDYYMMVNTWVFPVWYLLIIVCRACFPDQHGIVAMVLDYTS 77  
DB 124 TKKFEFLFVLDPADGWYRMLFLIALPVLYNMCILVARACFSDQKGYIWMVLDYVSD 183  
QY 78 LTVLLDMVVRPHFGFLEOGILVVDKGRISRYRTWSFELDASLMPDQVYVRLGPHTP 137  
DB 184 VVYIADLIIIRLRTGFLQGLLVKDPKCLRNYHTLQFKLDVASIIPDLIYFVAGIHNP 243  
QY 138 TLRLNRLRAPRLFEADRTETRTAYPNAPRIAKMLYIFVVIHNSCLYFALSRYLFG 197  
DB 244 EVRNRLHFRARMEFPDRTRTSYNPRIISMLYILIIHMACTIYVSKSIGFG 303  
QY 198 RDAWVYDPAQPGFERLRQYLYSFYSTLITLVGDTPPPAREEYLFVWGDPLAVMG 257  
DB 304 VDTWVYNNITDPEYGYLAREYIYCLYWSITLITIGETPPVDEYLFVFDLIGVLI 363  
QY 258 FATMGSMSSYIYMMNTADAAPFYPDHALVKKYMKLQHNKRLERRVIDWYQHLQINKMT 317  
DB 364 FATVGVNGSMISNMNATRAEFQAKIDAVGVHMQFRKYSKMEAKVIRWFDYLTNKKSV 423  
QY 318 NEVALIOLPERLRAEVAVSVHLSLTSRVQIFONCEASILEEVLKLOPQTSFGYVCR 377  
DB 424 DERIVLKNLPKLAELAINVHSLTKKVRIFQDCEAGLVEVLKLRPQVPSGDYICR 483  
QY 378 KGDIGQEMYIIRREGQLAVVADGGITQYAVLAGLYFGEISIIINIKMGSGRRRTANIKSL 437  
DB 484 KGDIGKEMYIIRKEGLAVVADGGITQYAVLAGLYFGEISIIINIKMGSGRRRTANIKSL 543  
QY 438 GYSDFCLSKEDLEEVSEYPOAQTIMEKREIILKNKLDVNAEAA--EIALQEATES 495  
DB 544 GYSDFCLSKDLEAVEYEPDAKVLBERGREILMKGLIDENBVAASMEVDVQE---- 599  
QY 496 RLRGDQQLDLDQTKFARLLAELESSALKIAYRIERLEMOTREMPMPEDLAADDEGP 554  
DB 600 KLEQLETMTDLYTRFARLLAEYGAQOKLKQKITVLETMKQNNEDDLSLSDGMSPEP 658

RESULT 15  
US-10-295-573-5  
Sequence 5, Application US/10295573  
Publication No. US20030157571A1  
GENERAL INFORMATION:  
APPLICANT: Rich, Jeffrey W.  
APPLICANT: Karpen, Jeffrey W.  
APPLICANT: Cooper, Dermot M.F.  
APPLICANT: Schack, Jerome  
TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS  
FILE REFERENCE: UNC-07536  
CURRENT APPLICATION NUMBER: US/10/295,573  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: 60/332,494  
PRIOR FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 664  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-295-573-5

Query Match 52.4%; Score 1565; DB 14; Length 664;  
Best Local Similarity 54.4%; Pred. No. 7.2e-135;  
Matches 293; Conservative 106; Mismatches 134; Indels 6; Gaps 2;

QY 18 SKARKLIPVLDPSGDYYMMVNTWVFPVWYLLIIVCRACFPDQHGIVAMVLDYTS 77  
DB 126 TKKFEFLFVLDPADGWYRMLFLVAMPVLYNMCILVARACFSDQKRYIYFVWVLDYFSD 185  
QY 78 LTVLLDMVVRPHFGFLEOGILVVDKGRISRYRTWSFELDASLMPDQVYVRLGPHTP 137  
DB 186 TVYIADLIIIRLRTGFLQGLLVKDPKCLRNYHTLQFKLDVASIIPDLIYFVAGIHNP 245  
QY 138 TLRLNRLRAPRLFEADRTETRTAYPNAPRIAKMLYIFVVIHNSCLYFALSRYLFG 197  
DB 246 EVRNRLHFRARMEFPDRTRTSYNPRIISMLYILIIHMACTIYVSKSIGFG 305  
QY 198 RDAWVYDPAQPGFERLRQYLYSFYSTLITLVGDTPPPAREEYLFVWGDPLAVMG 257  
DB 306 VDTWVYNNITDPEYGYLAREYIYCLYWSITLITIGETPPVDEYLFVFDLIGVLI 365  
QY 258 FATMGSMSSYIYMMNTADAAPFYPDHALVKKYMKLQHNKRLERRVIDWYQHLQINKMT 317  
DB 366 FATVGVNGSMISNMNATRAEFQAKIDAVGVHMQFRKYSKMEAKVIRWFDYLTNKKTV 425  
QY 318 NEVALIOLPERLRAEVAVSVHLSLTSRVQIFONCEASILEEVLKLOPQTSFGYVCR 377  
DB 426 DERIVLKNLPKLAELAINVHSLTKKVRIFQDCEAGLVEVLKLRPQVPSGDYICR 485  
QY 378 KGDIGQEMYIIRREGQLAVVADGGITQYAVLAGLYFGEISIIINIKMGSGRRRTANIKSL 437  
DB 486 KGDIGKEMYIIRKEGLAVVADGGITQYAVLAGLYFGEISIIINIKMGSGRRRTANIKSL 545  
QY 438 GYSDFCLSKEDLEEVSEYPOAQTIMEKREIILKNKLDVNAEAA--EIALQEATES 495  
DB 546 GYSDFCLSKDLEAVEYEPDAKVLBERGREILMKGLIDENBVAASMEVDVQE---- 601  
QY 496 RLRGDQQLDLDQTKFARLLAELESSALKIAYRIERLEMOTREMPMPEDLAADDEGP 554  
DB 602 KLEQLETMTDLYTRFARLLAEYGAQOKLKQKITVLETMKQNNEDDLSLSDGINTPEP 660

Search completed: September 11, 2004, 01:49:05  
Job time : 455 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: September 10, 2004, 20:16:54 ; Search time 803.203 seconds  
(without alignments)  
10824.747 Million cell updates/sec

Title: US-09-927-267-3

Perfect score: 1728

Sequence: 1 atgagccaggacacaaagt.....gaccccgagtcagagtgta 1728

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
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18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	1728	9	US-09-927-267-3
2	1728	100.0	1728	16	US-10-189-507-2
3	1728	100.0	2308	9	US-09-927-267-2
4	1728	100.0	2366	13	US-10-302-172-351
5	1726.4	99.9	2013	17	US-10-311-624-2
6	1726.4	99.9	2551	10	US-09-842-758-29
7	1726.4	99.9	2551	13	US-10-174-333-29
8	1721.6	99.6	1758	9	US-09-735-932-1
9	1721.6	99.6	1758	15	US-10-207-951-1
10	1687.4	97.7	1835	13	US-09-842-758-27
11	1687.4	97.7	1835	10	US-10-174-333-27
12	652.6	37.8	10989	9	US-09-735-932-3
13	652.6	37.8	10989	15	US-10-207-951-3
14	588.2	34.0	2085	15	US-10-345-680-27

15	588.2	34.0	3486	15	US-10-345-680-25	Sequence 25, Appl
16	580.2	33.6	1995	9	US-09-735-927-1	Sequence 1, Appl
17	580.2	33.6	1995	16	US-10-189-507-4	Sequence 4, Appl
18	578.6	33.5	1995	14	US-10-034-843-1	Sequence 1, Appl
19	578.6	33.5	1995	15	US-10-168-651-34	Sequence 34, Appl
20	578.6	33.5	1995	16	US-10-189-507-1	Sequence 1, Appl
21	578.6	33.5	2111	15	US-10-114-153-17	Sequence 17, Appl
22	578.6	33.5	2130	15	US-10-029-677-23	Sequence 23, Appl
23	577	33.4	2186	15	US-10-029-677-1	Sequence 1, Appl
24	534.8	30.9	3027	15	US-10-295-573-1	Sequence 1, Appl
25	533.2	30.9	1995	15	US-10-087-217-5	Sequence 5, Appl
26	533.2	30.9	3027	15	US-10-295-573-2	Sequence 2, Appl
27	530	30.7	1995	15	US-10-087-217-1	Sequence 1, Appl
28	530	30.7	1995	15	US-10-087-217-7	Sequence 7, Appl
29	530	30.7	3027	15	US-10-295-573-4	Sequence 4, Appl
30	526.8	30.5	1995	15	US-10-087-217-3	Sequence 3, Appl
31	514.2	29.8	2877	15	US-10-295-573-3	Sequence 3, Appl
32	498.6	28.9	12017	9	US-09-735-927-3	Sequence 3, Appl
33	452.4	26.2	2500	13	US-10-342-887-427	Sequence 427, App
34	452.4	26.2	2500	13	US-10-172-118-427	Sequence 427, App
35	370.6	21.4	601	15	US-10-207-951-24	Sequence 24, Appl
36	124.8	7.2	2607	16	US-10-189-507-3	Sequence 3, Appl
37	124.8	7.2	4382	16	US-10-159-563-147	Sequence 147, App
38	99	5.7	470	13	US-10-085-783A-42809	Sequence 42809, A
39	99	5.7	470	16	US-10-242-535A-42809	Sequence 42809, A
40	89.2	5.2	4751	13	US-10-311-795-5	Sequence 5, Appl
41	89.2	5.2	5065	15	US-10-067-457-4	Sequence 4, Appl
42	89.2	5.2	5489	13	US-10-276-774-973	Sequence 973, App
43	79	4.6	2430	12	US-09-855-828-3	Sequence 3, Appl
44	79	4.6	2703	12	US-09-855-828-2	Sequence 2, Appl
45	79	4.6	2757	12	US-09-855-828-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-927-267-3  
; Sequence 3, Application US/09927267  
; Publication No. US20020182691A1  
; GENERAL INFORMATION:  
; APPLICANT: Creech, Christopher D.  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: ICGen, Inc.  
; TITLE OF INVENTION: CNG2B: A No. US20020182691A1el Human Cyclic Nucleotide-Gated Ion  
; FILE REFERENCES: 018512-006510US  
; CURRENT APPLICATION NUMBER: US/09/927,267  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/226,253  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)  
; NAME/KEY: CDS  
; LOCATION: (1)..(1728)  
; OTHER INFORMATION: CNG2B  
; US-09-927-267-3

Query Match 100.0%; Score 1728; DB 9; Length 1728;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCCAGGACCAAGTGAAGCAAGAGTCCAGTCCCGCCCGCCCATCAAGGCC 60  
DB 1 ATGAGCCAGGACCAAGTGAAGCAAGAGTCCAGTCCCGCCCGCCCATCAAGGCC 60

QY	61	AGGAAGTTGCTGCGCTGCTGTCGACCCGATCTGCGGGATTAATCACTCACTGCTGGCTGAACACA	120
Dp	61	AGGAAGTTGCTGCTGCTGCTGTCGACCCGATCTGCGGGATTAATCACTCACTGCTGGCTGAACACA	120
QY	121	ATGGCTCTCCAGTCATGATATTAACCTCATCTCGTGTGACAGAGCCCTGTTCCCGAC	180
Dp	121	ATGGCTCTCCAGTCATGATATTAACCTCATCTCGTGTGACAGAGCCCTGTTCCCGAC	180
QY	181	TTTGACGACCGGTTATCTGCTGCGCTGGTGGTGTGCTGGACTTACACAGATGACCTGTCTATAC	240
Dp	181	TTTGACGACCGGTTATCTGCTGCGCTGGTGGTGTGCTGGACTTACACAGATGACCTGTCTATAC	240
QY	241	CTACTAGACATGCTGCTGCTGCTTCCACACAGATTTCTTGGAAACAGGCAATCCTGTGATG	300
Dp	241	CTACTAGACATGCTGCTGCTGCTTCCACACAGATTTCTTGGAAACAGGCAATCCTGTGATG	300
QY	301	GACAAAGGTAGGATCTCGAGTCGCTACGCTTGCGACTTGGAAGTTTCTTCTTGAGACTGACT	360
Dp	301	GACAAAGGTAGGATCTCGAGTCGCTACGCTTGCGACTTGGAAGTTTCTTCTTGAGACTGACT	360
QY	361	TCCCTGATGCCCAAGATGTGTCTACGTGGGCTGGGACCCGACACACCCACTTGAG	420
Dp	361	TCCCTGATGCCCAAGATGTGTCTACGTGGGCTGGGACCCGACACACCCACTTGAG	420
QY	421	CTGAACCGCTTCTCCGCGCGCCCGGCTTCTCGAAGGCTTCGACCGGACAGAGACCCG	480
Dp	421	CTGAACCGCTTCTCCGCGCGCCCGGCTTCTCGAAGGCTTCGACCGGACAGAGACCCG	480
QY	481	ACAGCTTACCCMAATGCTTTGCAATGTCGACAGCTGATGCTTTACATTTTGTGCTATC	540
Dp	481	ACAGCTTACCCMAATGCTTTGCAATGTCGACAGCTGATGCTTTACATTTTGTGCTATC	540
QY	541	CATTGGAACAGCTGCTTATCTTTGCGCTATCCCGGTACCTGGGCTTGGGCGTGAAGCA	600
Dp	541	CATTGGAACAGCTGCTTATCTTTGCGCTATCCCGGTACCTGGGCTTGGGCGTGAAGCA	600
QY	601	TGGGTATCCCGGACCCCGCGAGCTGTGACTTGAAGGCTTGGCGGCGCACTACTCTAT	660
Dp	601	TGGGTATCCCGGACCCCGCGAGCTGTGACTTGAAGGCTTGGCGGCGCACTACTCTAT	660
QY	661	AGCTTTTACTTCTCCACGCTGATACTGACTCAGTGGGCGATGACACGCGCCGACGACG	720
Dp	661	AGCTTTTACTTCTCCACGCTGATACTGACTCAGTGGGCGATGACACGCGCGCCGACGACG	720
QY	721	GAAAGAAGTACCTTCTTATGTGTGGGCACTTCTGCTGCGCGGTATGGTGTGGCAAC	780
Dp	721	GAAAGAAGTACCTTCTTATGTGTGGGCACTTCTGCTGCGCGGTATGGTGTGGCAAC	780
QY	781	ATCATGGGTACATGAGCTCTGTATCATATCAACAATGAAACCTGCGAGATCGGCTTTCTAC	840
Dp	781	ATCATGGGTACATGAGCTCTGTATCATATCAACAATGAAACCTGCGAGATCGGCTTTCTAC	840
QY	841	CCAGATCATGCACTGTGTGAGAAAGTACATGAAGCTGACGACGTCAACCGCAAGCTGGAG	900
Dp	841	CCAGATCATGCACTGTGTGAGAAAGTACATGAAGCTGACGACGTCAACCGCAAGCTGGAG	900
QY	901	CGGCGAGTTATTTGACTGTGTATCAGCACTGAGATCAACAAAGATGACCAAGAGGTA	960
Dp	901	CGGCGAGTTATTTGACTGTGTATCAGCACTGAGATCAACAAAGATGACCAAGAGGTA	960
QY	961	GCAATCTTACAGCACTTGTGCGAGGGGTGGGGGAGAAAGTGGGCTGTGTCGACCTG	1020
Dp	961	GCAATCTTACAGCACTTGTGCGAGGGGTGGGGGAGAAAGTGGGCTGTGTCGACCTG	1020
QY	1021	TCCACTCTGAGCGCGGGTGCAGATCTTTACAAACTGTGAGGCGAGCTGTGAGAGAGCTG	1080
Dp	1021	TCCACTCTGAGCGCGGGTGCAGATCTTTACAAACTGTGAGGCGAGCTGTGAGAGAGCTG	1080
QY	1081	GTGCTGAAGCTGCAAGCCCGACGCTACTCACAGGTGAATATGTATGTCGCGAAAGGAAAC	1140
Dp	1081	GTGCTGAAGCTGCAAGCCCGACGCTACTCACAGGTGAATATGTATGTCGCGAAAGGAAAC	1140
QY	1141	ATTGGCCCAAGAGATATATCATCTCCGAAGGCTCACTGCGCGTGTGGACAGATGATGCT	1200

Db	1141	ATTGGCCAAAGATGTATCATTCATCCGAGAGGGTCAATGGGCCCGGTGGCAGATGATG3T	1200
QY	1201	ATCACACAGTATGCTGTGCTCGGTGCAGGGCTCTACTTTGGGGAGTACAGATCATTAAC	1260
Db	1201	ATCACACAGTATGCTGTGCTCGGTGCAGGGCTCTACTTTGGGGAGTACAGATCATTAAC	1260
QY	1261	ATCAAAAGGAACATGTGTGGGAAACCGCCGACACAGCCAAATCAAGACCTTAGTTATTCA	1320
Db	1261	ATCAAAAGGAACATGTGTGGGAAACCGCCGACACAGCCAAATCAAGACCTTAGTTATTCA	1320
QY	1321	GACCTATTCTGCTCGACCAAGAGAGACTTGCGGAGGTGCTGACGAGTATCCACAAGCA	1380
Db	1321	GACCTATTCTGCTCGACCAAGAGAGACTTGCGGAGGTGCTGACGAGTATCCACAAGCA	1380
QY	1381	CAGGCCATTCATGGAGGAGAAAGACGTGAGATCCTGTGTAATAATGAACAAGTTGAGCGTG	1440
Db	1381	CAGGCCATTCATGGAGGAGAAAGACGTGAGATCCTGTGTAATAATGAACAAGTTGAGCGTG	1440
QY	1441	AATGCTGAGGACAGCTGAGATCGCCCTGCAGAGGCCACAGAGTCCCGGCTACGAGGCTTA	1500
Db	1441	AATGCTGAGGACAGCTGAGATCGCCCTGCAGAGGCCACAGAGTCCCGGCTACGAGGCTTA	1500
QY	1501	GACCAAGACGTGATATCTACAGACCAAGTTTGCTGCTCCTCGGCTGAGCTGAGATGCC	1560
Db	1501	GACCAAGACGTGATATCTACAGACCAAGTTTGCTGCTCCTCGGCTGAGCTGAGATGCC	1560
QY	1561	AGGCCACTTAAGATTGCTTACCCGATTTGAACCGCTGAGAGTGGCAGACTTCGAGATGGCCA	1620
Db	1561	AGGCCACTTAAGATTGCTTACCCGATTTGAACCGCTGAGAGTGGCAGACTTCGAGATGGCCA	1620
QY	1621	ATGCCCCGAGGACCTGCGCTGAGGCTGATGACGAGGGTGAAGCTTGAGAGGGAACTTCCAAA	1680
Db	1621	ATGCCCCGAGGACCTGCGCTGAGGCTGATGACGAGGGTGAAGCTTGAGAGGGAACTTCCAAA	1680
QY	1681	GATTAACAAGGCGAAGGCGACGACCAAGAGAGGCCCCCAAGTCCAGAGTGA 1728	
Db	1681	GATTAACAAGGCGAAGGCGACGACCAAGAGAGGCCCCCAAGTCCAGAGTGA 1728	

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RESULT 2
US-10-189-507-2
; Sequence 2, Application US/10189507
; Publication No. US20030228633A1
GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEXY
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
APPLICANT: CALAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; TITLE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-189-507-2
Query Match 100.0%; Score 1728; DB 16; Length 1728;

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LOCATION: (333)..(2060)  
OTHER INFORMATION: CMG2B  
US-09-927-267-2

Query Match 100.0%; Score 1728; DB 9; Length 2308;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 333 ATGAGCCAGGACACCAAGTGAAGACAAACAGATCCAGTCCCGCCAGCCCTCCAGAGCC 392
QY 61 AGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 393 AGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452
QY 121 ATGATCTTCCAGTATGATATATACCTCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 453 ATGATCTTCCAGTATGATATATACCTCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 512
QY 181 TTGACAGACGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 513 TTGACAGACGGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
QY 241 CTACTAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 573 CTACTAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
QY 301 GACAAAGGATGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 633 GACAAAGGATGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
QY 361 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 693 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
QY 421 CTGAAACCGCTTCTTCCGCGGCGCCGCGCTTCTGAGGCTTCTGAGCCGCAAGAGACCCGC 480
DB 753 CTGAAACCGCTTCTTCCGCGGCGCCGCGCTTCTGAGGCTTCTGAGCCGCAAGAGACCCGC 812
QY 481 ACAGCTTACCCAAATGCTTCCGATTCGCAATGCTTACATTTTGTGCTATC 540
DB 813 ACAGCTTACCCAAATGCTTCCGATTCGCAATGCTTACATTTTGTGCTATC 872
QY 541 CATGGAAGAGCTGCTTCTTCCGATTCGCAATGCTTACATTTTGTGCTATC 600
DB 873 CATGGAAGAGCTGCTTCTTCCGATTCGCAATGCTTACATTTTGTGCTATC 932
QY 601 TGGGTGTACCCGACCCCGCGCAGCTTGTGAGCGCTGCGGCGCAGTACCTTAT 660
DB 933 TGGGTGTACCCGACCCCGCGCAGCTTGTGAGCGCTGCGGCGCAGTACCTTAT 992
QY 661 AGCTTTTACTTCTTCCAGCTGATCTACTACATGAGGCGATACACCGCCGCCAGCAGG 720
DB 993 AGCTTTTACTTCTTCCAGCTGATCTACTACATGAGGCGATACACCGCCGCCAGCAGG 1052
QY 721 GAAGAAGAGTACCTTCTTCCAGCTGAGGAGCTTCTGCTGCGCGCATGAGGTTTCCGACC 780
DB 1053 GAAGAAGAGTACCTTCTTCCAGCTGAGGAGCTTCTGCTGCGCGCATGAGGTTTCCGACC 1112
QY 781 ATCATGGGTAGCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 1113 ATCATGGGTAGCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
QY 841 CCAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 1173 CCAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
QY 901 CGCGAGATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1233 CGCGAGATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
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DB 1293 GCCATCTTACAGCATTTGCTGAGCGGCTGCGGCGAGAGTGTGCTGTGCTGCTGCTGCTGCTGCT 1352
QY 1021 TCCATCTGAGCCCGGCTGAGATCTTTCAGAACTGTGAGGCGACCTGCTGAGAGGCTG 1080
DB 1353 TCCATCTGAGCCCGGCTGAGATCTTTCAGAACTGTGAGGCGACCTGCTGAGAGGCTG 1412
QY 1081 GTGCTGAGCTGAGCCCGGCTGAGATCTTTCAGAACTGTGAGGCGACCTGCTGAGAGGCTG 1140
DB 1413 GTGCTGAGCTGAGCCCGGCTGAGATCTTTCAGAACTGTGAGGCGACCTGCTGAGAGGCTG 1472
QY 1141 ATTGCGCAAGAGATGATCATCATCTGAGAGGCTGCTGAGGCGGCTGCTGAGAGGCTGCTGAG 1200
DB 1473 ATTGCGCAAGAGATGATCATCATCTGAGAGGCTGCTGAGGCGGCTGCTGAGAGGCTGCTGAG 1532
QY 1201 ATCAGACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1533 ATCAGACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1592
QY 1261 ATCAAAGGAAACATGCTGAGGAAACCGCGCAAGCCCAACATCAGAGCTTATGTTATTC 1320
DB 1593 ATCAAAGGAAACATGCTGAGGAAACCGCGCAAGCCCAACATCAGAGCTTATGTTATTC 1652
QY 1321 GACCTATTTGCTGCTGAGCAAGAGGACCTGCGGAGGCTGCTGAGCGGATTCACAGCA 1380
DB 1653 GACCTATTTGCTGCTGAGCAAGAGGACCTGCGGAGGCTGCTGAGCGGATTCACAGCA 1712
QY 1381 CAGACCATCATGAGAGGAAAGGACGTGAGATCTGCTGAAATGAACAAAGTTGAGCGTG 1440
DB 1713 CAGACCATCATGAGAGGAAAGGACGTGAGATCTGCTGAAATGAACAAAGTTGAGCGTG 1772
QY 1441 AATGCTGAGGACGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1773 AATGCTGAGGACGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1832
QY 1501 GACCAGAGCTGATGATCTACAGACCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1833 GACCAGAGCTGATGATCTACAGACCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1892
QY 1561 AGGCACTTAAGATGCTTACCCGATTTGAACGCTGAGTGGGCACTGAGAGTGGCCA 1620
DB 1893 AGGCACTTAAGATGCTTACCCGATTTGAACGCTGAGTGGGCACTGAGAGTGGCCA 1952
QY 1621 ATGCCGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1953 ATGCCGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2012
QY 1681 GATGAAGAGGCGAGGCGCAGCCAGAGGAGGACCCCAAGTCCAGAGTGA 1728
DB 2013 GATGAAGAGGCGAGGCGCAGCCAGAGGAGGAGGACCCCAAGTCCAGAGTGA 2060

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RESULT 4
US-10-302-172-351
; Sequence 351, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aiding J.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
; FILE REFERENCE: 803.1CNDP
; CURRENT APPLICATION NUMBER: US/10/302.172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_genes Version 2.0

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incycle ID No: 6703242CB1
US-10-311-624-2

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Query Match      99.9%; Score 1726.4; DB 17; Length 2013;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1727; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGAGCCAGGACCCAAAGTGAAGACAAAGAGTCCAGTCCCGAGCCCATCCAAAGCC 60
DB 124 ATAGCCAGGACACCAAGTGAAGACAAAGAGTCCCGAGCCCATCCAAAGCC 183
QY 61 AGGAAGTGTGCTGCTGCTCTGAGCCCATCTGGGATTACTACTGTGGTGAACACA 120
DB 184 AGGAAGTGTGCTGCTGCTCTGAGCCCATCTGGGATTACTACTGTGGTGAACACA 243
QY 121 ATGCTCTTCCAGTCTATGTTAACTTATATCTCTGTGTGAGAGCTTCTCCGAC 180
DB 244 ATGCTCTTCCAGTCTATGTTAACTTATATCTCTGTGTGAGAGCTTCTCCGAC 303
QY 181 TTGACAGAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 304 TTGACAGAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
QY 241 CTACTAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 364 CTACTAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
QY 301 GACAAAGGTTAGATCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 424 GACAAAGGTTAGATCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 361 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 484 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 421 CTGAACCGCTTCTCCGCGCGCCCGCTCTTGAAGGCTTCCAGCGCAGAGACCCG 480
DB 544 CTGAACCGCTTCTCCGCGCGCCCGCTCTTGAAGGCTTCCAGCGCAGAGACCCG 603
QY 481 AAGGCTTACCCAAATGCTTGTGCAATTCGCAAGCTGATGCTTAACTTTTGTGCTATC 540
DB 604 AAGGCTTACCCAAATGCTTGTGCAATTCGCAAGCTGATGCTTAACTTTTGTGCTATC 663
QY 541 CATTGGAACAGCTGCTTATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 664 CATTGGAACAGCTGCTTATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
QY 601 TGGGTGTACCCGAGACCCCGCGAGCTGCTTGAAGGCTGCTGCTGCTGCTGCTGCT 660
DB 724 TGGGTGTACCCGAGACCCCGCGAGCTGCTTGAAGGCTGCTGCTGCTGCTGCTGCT 783
QY 661 AGCTTTTACTTCTCAACGCTGATGATGATGATGATGATGATGATGATGATGATG 720
DB 784 AGCTTTTACTTCTCAACGCTGATGATGATGATGATGATGATGATGATGATGATG 843
QY 721 GAAGAAGAGTACCTCTTCAATGAGGCGACTTCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 844 GAAGAAGAGTACCTCTTCAATGAGGCGACTTCTGCTGCTGCTGCTGCTGCTGCTG 903
QY 781 ATCATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 904 ATCATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 963
QY 841 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900

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DB 964 CCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1023
QY 901 CGGCGAGTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 1024 CGGCGAGTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083
QY 961 GGCATCTTACAGCATTTGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAG 1020
DB 1084 GGCATCTTACAGCATTTGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAG 1143
QY 1021 TCCACTCTGAGCGCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGG 1080
DB 1144 TCCACTCTGAGCGCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGG 1203
QY 1081 GTGCTGAAGCTGAGGCGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT 1140
DB 1204 GTGCTGAAGCTGAGGCGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCT 1263
QY 1141 ATTGGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1264 ATTGGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323
QY 1201 ATCAACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1324 ATCAACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1383
QY 1261 ATCAAGGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1384 ATCAAGGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
QY 1321 GACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1444 GACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1503
QY 1381 CAGACCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
DB 1504 CAGACCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563
QY 1441 AATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
DB 1564 AATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1623
QY 1501 GACGACGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
DB 1624 GACGACGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1683
QY 1561 AGCGCATTAAGATTTGCTTACCGCATTTGAAGGCTGAGGAGGAGGAGGAGGAG 1620
DB 1684 AGCGCATTAAGATTTGCTTACCGCATTTGAAGGCTGAGGAGGAGGAGGAGGAG 1743
QY 1621 ATGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
DB 1744 ATGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1803
QY 1681 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1728
DB 1804 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1851

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RESULT 6  
US-09-842-758-29

; Sequence 29, Application US/09842758

; Publication No. US20030083244A1

; GENERAL INFORMATION:

; APPLICANT: Vermet, Corine A. M.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Shinkels, Richard A

; APPLICANT: Mal'yankar, Uriel M

; APPLICANT: Boldog, Ferenc L

; APPLICANT: Zeinhusen, Bryan D

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Majumder, Kumud

						APPLICANT: Tcherney, Velizar T
						APPLICANT: Padigarau, Muralidhara
						APPLICANT: Patuturajan, Neera
						APPLICANT: Burgess, Catherine E
						APPLICANT: Gangoli, Esha A
						APPLICANT: Smithson, Glenna
						APPLICANT: Rastelli, Luca
						APPLICANT: MacDougall, John R
						APPLICANT: Taupier, Raymond J
						APPLICANT: Grose, William M
						APPLICANT: Edward, Szekeres S
						APPLICANT: Alsbrook II, John P
						TITLE OF INVENTION: No. US20030089324A1el Proteins and Nucleic Acids Encoding Same
						FILE REFERENCE: 1566-783
						CURRENT APPLICATION NUMBER: US/09/842,758
						CURRENT FILING DATE: 2001-04-25
						PRIOR APPLICATION NUMBER: 60/200,158
						PRIOR FILING DATE: 2000-04-26
						PRIOR APPLICATION NUMBER: 60/200,613
						PRIOR FILING DATE: 2000-04-28
						PRIOR APPLICATION NUMBER: 60/200,780
						PRIOR FILING DATE: 2000-04-28
						PRIOR APPLICATION NUMBER: 60/201,006
						PRIOR FILING DATE: 2000-05-01
						PRIOR APPLICATION NUMBER: 60/201,007
						PRIOR FILING DATE: 2000-05-01
						PRIOR APPLICATION NUMBER: 60/201,236
						PRIOR FILING DATE: 2000-05-01
						PRIOR APPLICATION NUMBER: 60/201,238
						PRIOR FILING DATE: 2000-05-01
						PRIOR APPLICATION NUMBER: 60/201,186
						PRIOR FILING DATE: 2000-05-02
						PRIOR APPLICATION NUMBER: 60/201,474
						PRIOR FILING DATE: 2000-05-03
						PRIOR APPLICATION NUMBER: 60/201,508
						PRIOR FILING DATE: 2000-05-03
						PRIOR APPLICATION NUMBER: 60/220,591
						PRIOR FILING DATE: 2000-07-25
						PRIOR APPLICATION NUMBER: 60/232,678
						PRIOR FILING DATE: 2000-09-15
						PRIOR APPLICATION NUMBER: 60/263,217
						PRIOR FILING DATE: 2001-01-22
						PRIOR APPLICATION NUMBER: 60/265,160
						PRIOR FILING DATE: 2001-01-30
						NUMBER OF SEQ ID NOS: 113
						SOFTWARE: PatentIn Ver. 2.1
						SEQ ID NO 29
						LENGTH: 2551
						TYPE: DNA
						ORGANISM: Homo sapiens
						US-09-842-758-29
Query Match		99.9%	Score 1726.4;	DB 10;	Length 2551;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 1727; Conservative		0;	Mismatches	1;	Indels	0;
Gaps		0;				
OY	1	ATGAGCCGACGACCAAAAGTGAACAACAAGATGCCAGTCCCCAGCCCATCCAAGGC	60			
Db	779	ATGAGCCGACGACCAAAAGTGAACAACAAGATGCCAGTCCCCAGCCCATCCAAGGC	838			
OY	61	AGGAAGTTGTGGCTTCCTTGCGTAGCACCATTGGGGGATTAATACTACTAGTGTGGCTGAACA	120			
Db	839	AGGAAGTTGTGGCTTCCTTGCGTAGCACCATTGGGGGATTAATACTACTAGTGTGGCTGAACA	898			
OY	121	ATGCTCTTCCCAGTCATGTATTAACCTCATATCTCTGCTGTGCAGAAGCTGTTCCCGCAC	180			
Db	899	ATGCTCTTCCCAGTCATGTATTAACCTCATATCTCTGCTGTGCAGAAGCTGTTCCCGCAC	958			
OY	181	TTGACAGCAGGTTATCTGTGTGGCTGTGTGTGTGTGACATPACAGAGTGAAGCTGCTATAC	240			
Db	959	TTGACAGCAGGTTATCTGTGTGGCTGTGTGTGTGTGACATPACAGAGTGAAGCTGCTATAC	1018			
OY	241	CTACTAGCATGTGTGTGCGCTTCACACAGAGATTTCTTGAACAGGGCATTCGTGTGTG	300			

Db	1019	CTACTGACATGAGTGGTGCCTTCCACACAGGATTTCTTGAAACAGGGATCTGTGGTGTG	1078
QY	301	GACAAAGGGTAGAGATCTGAGAGCGCTACGTTGCGACCTGAGATTCTTCTTGAGACCTGGACT	360
Db	1079	GACAAAGGGTAGAGATCTGAGAGCGCTACGTTGCGACCTGAGATTCTTCTTGAGACTGGCT	1138
QY	361	TCCTGTATGCCACAGATGTGTGTCTACGTGCGGTGGGCCCGGACACACCCACCCTGAGG	420
Db	1139	TCCCTGTATGCCACAGATGTGTGTCTACGTGCGGTGGGCCCGGACACACCCACCCTGAGG	1198
QY	421	CTGAACCGCTTCTCCGGCGGCCCCGCTCTTGCAGAGCTTTCGACCGGACAGAACCCGC	480
Db	1199	CTGAACCGCTTCTCCGGCGGCCCCGCTCTTGCAGAGCTTTCGACCGGACAGAACCCGC	1258
QY	481	ACAGCTTACCCAAATGCGCTTGCATTGGCCAAAGCTGATGCTTTACATTTTGTGTGTCATC	540
Db	1259	ACAGCTTACCCAAATGCGCTTTCGATTGGCCAAAGCTGATGCTTTACATTTTGTGTGTCATC	1318
QY	541	CATTGGAACAGCTGCTTATACCTTTGCCCTATCCCGGTACCTGGGCTTTCGGCGCTGACGCA	600
Db	1319	CATTGGAACAGCTGCTTATACCTTTGCCCTATCCCGGTACCTGGGCTTTCGGCGCTGACGCA	1378
QY	601	TGGGTGTATCCCGGACCCCGCGACCTTGGCTTTAGGGCTCTGGCGCCAGTACCTCTAT	660
Db	1379	TGGGTGTATCCCGGACCCCGCGACCTTGGCTTTAGGGCTCTGGCGCCAGTACCTCTCTAT	1438
QY	661	AGCTTTTACTTCTGCAAGCTGATACCTGACACTACAGTGGGGCGATTACACCGCCGCGACGAG	720
Db	1439	AGCTTTTACTTCTGCAAGCTGATACCTGACACTACAGTGGGGCGATTACACCGCCGCGACGAG	1498
QY	721	GAAAGAAGATACCTTTCATGTGTGGGAGACTTCCGTGCGCGCTGATGATGGTTTGCGACAC	780
Db	1499	GAAAGAAGATACCTTTCATGTGTGGGAGACTTCCGTGCGCGCTGATGATGGTTTGCGACAC	1558
QY	781	ATCATGGGTAGCATGAGCTCTGTATCTTACAACTGAACTGACATGCGGCTTTTCTAC	840
Db	1559	ATCATGGGTAGCATGAGCTCTGTATCTTACAACTGAACTGACATGCGGCTTTTCTAC	1618
QY	841	CCAATCATGACACTGTGTGAAGAATCTATCATGAAGCTGACAGACCTGCAACCCGACCTGGAG	900
Db	1619	CCAATCATGACACTGTGTGAAGAATCTATCATGAAGCTGACAGACCTGCAACCCGACCTGGAG	1678
QY	901	CGCGAGTTATTGACTGTATCTGATCTCAGCACTCGACATCAACAAGATGATCCAAAGAGSTA	960
Db	1679	CGCGAGTTATTGACTGTATCTGATCTCAGCACTCGACATCAACAAGATGATCCAAAGAGSTA	1738
QY	961	GCCATCTTTACAGCACTTGCTGAGCGGCTGCGGCAAAAGTGTGTGTGTGCACCTG	1020
Db	1739	GCCATCTTTACAGCACTTGCTGAGCGGCTGCGGCAAAAGTGTGTGTGTGCACCTG	1798
QY	1021	TTCGACTCTGAGCGCGGTGACGATCTTTTCAGAACTGTGAGGCGACCTGTGTGAAGAGCTG	1080
Db	1799	TTCGACTCTGAGCGCGGTGACGATCTTTTCAGAACTGTGAGGCGACCTGTGTGAAGAGCTG	1858
QY	1081	GTGCTGAAGCTGACGCCCAAGACTTATCTCACAAGTGAATATGTATGCTCCGCAAGAGGAC	1140
Db	1859	GTGCTGAAGCTGACGCCCAAGACTTATCTCACAAGTGAATATGTATGCTCCGCAAGAGGAC	1918
QY	1141	ATTGGCCAAAGATGTACATCATCCGAGAGGGTCAACTGTGCGTGTGGCGAGATGATGTGT	1200
Db	1919	ATTGGCCAAAGATGTACATCATCCGAGAGGGTCAACTGTGCGTGTGTGGCGAGATGATGTGT	1978
QY	1201	ATTCACACAGTATGCTGTGCTGCGGTGACAGGGCTGTCATTTGGGGAGATCAGATCATCAAC	1260
Db	1979	ATTCACACAGTATGCTGTGCTGCGGTGACAGGGCTGTCATTTGGGGAGATCAGATCATCAAC	2038
QY	1261	ATCAAAAGGAACATGTCTGGGAACCGCGCGACAGCCAAATCAAGAGCTTATGTTATTCA	1320
Db	2039	ATCAAAAGGAACATGTCTGGGAACCGCGCGACAGCCAAATCAAGAGCTTATGTTATTCA	2098
QY	1321	GACCTATTTTGTCTGAGCAAGAGGACCTTGCGGAGGTGTCTGACCGAGTATCCACAAGCA	1380



Dp	1499	GAAGAGAGTACTCTCTTACATGCTGGGACCATCTTCCTGCGCCCTCATGGGTTTGGCCAC	1558
Qy	781	ATCATGGGATGACATGAAGCTCTGTCACTTTCACATGAAACACTGCAGATGCGGCTTTCTAC	840
Dp	1559	ATCATGGGATGACATGAAGCTGTGTCACTTTCACATGAAACACTGCAGATGCGGCTTTCTAC	1618
Qy	841	CCAGATCATGCACTGGTGTGAAGAAAGTACATGAAAGCTGCAGACGCTTAACCCGAAGTGGAG	900
Dp	1619	CCAGATCATGCACTGGTGTGAAGAAAGTACATGAAAGCTGCAGACGCTTAACCCGAAGTGGAG	1678
Qy	901	CGGCGAGTTATGACTGTGATCAGCACTGCAGATCAACCAAGAAATGATACCAACGAGGTA	960
Dp	1679	CGGCGAGTTATGACTGTGATCAGCACTGCAGATCAACCAAGAAATGATACCAACGAGGTA	1738
Qy	961	GCCATCTTTACAGCACTTGCTGAGCGGCTGCGGCGAGAAAGTGGCTGTCTGTGCACCTG	1020
Dp	1739	GCCATCTTTACAGCACTTGCTGAGCGGCTGCGGCGAGAAAGTGGCTGTCTGTGCACCTG	1798
Qy	1021	TCCATCTGAGCGCGGGTGGAGTCTTTGAGAACTGTGAGGCCAGGCTTCTGTGAGAGCTG	1080
Dp	1799	TCCATCTGAGCGCGGGTGGAGTCTTTGAGAACTGTGAGGCCAGGCTTCTGTGAGAGCTG	1858
Qy	1081	GTGCTGAAGCTGCAACCCCGACACTACTCACCAGGTGATATGTAATGCGCGAAAGAGAC	1140
Dp	1859	GTGCTGAAGCTGCAACCCCGACACTACTCACCAGGTGATATGTAATGCGCGAAAGAGAC	1918
Qy	1141	ATTGGCCAAAGATGTATACATCATCCGAGAGGTCATCTGCCGTGTGTGGCAGATGATGCT	1200
Dp	1919	ATTGGCCAAAGATGTATACATCATCCGAGAGGTCATCTGCCGTGTGTGGCAGATGATGCT	1978
Qy	1201	ATCACACAGTATGCTGCTCGGTGCAGGGCTCATCTTGGGGAGATCAGATCATCAAC	1260
Dp	1979	ATCACACAGTATGCTGCTCGGTGCAGGGCTCATCTTGGGGAGATCAGATCATCAAC	2038
Qy	1261	ATCAAAAGGAAACATGTCTGGGAAACCGCCGACAGCCAACTCAAGAGCCTAGTTATTCA	1320
Dp	2039	ATCAAAAGGAAACATGTCTGGGAAACCGCCGACAGCCAACTCAAGAGCCTAGTTATTCA	2098
Qy	1321	GACCTATTCTGCTGAGCAAGAGGAACTCTGGGAGGCTGTGAGCGAGTATCCACAAACA	1380
Dp	2099	GACCTATTCTGCTGAGCAAGAGGAACTCTGGGAGGCTGTGAGCGAGTATCCACAAACA	2158
Qy	1381	CAGACCATCATGAGAGGAGAAAGACGTAGATCTGCTGAATAATGAACAATTGGAAGTG	1440
Dp	2159	CAGACCATCATGAGAGGAGAAAGACGTAGATCTGCTGAATAATGAACAATTGGAAGTG	2218
Qy	1441	AATGCTGAGGAGCTGAGATGCGCCTGCAGAGGCCACAGAGTCCCGGCTTACGAGGCTTA	1500
Dp	2219	AATGCTGAGGAGCTGAGATGCGCCTGCAGAGGCCACAGAGTCCCGGCTTACGAGGCTTA	2278
Qy	1501	GACCAAGACGCTGAGATGATCTTACAGAACCAAGTTTGTGCTGCTCTGAGCTGAGTCC	1560
Dp	2279	GACCAAGACGCTGAGATGATCTTACAGAACCAAGTTTGTGCTGCTCTGAGCTGAGTCC	2338
Qy	1561	AGGCACACTTAAGATTGCTTACCGGATTTGAACGGCTGAGATGGGAGACTCCGAGATGGCCA	1620
Dp	2339	AGGCACACTTAAGATTGCTTACCGGATTTGAACGGCTGAGATGGGAGACTCCGAGATGGCCA	2398
Qy	1621	ATGCCCGAGGACCTGGCTGAGGCTTGATGACGAGGGTAGACTGAGAGAGGAACTTCCAAA	1680
Dp	2399	ATGCCCGAGGACCTGGCTGAGGCTTGATGACGAGGGTAGACTGAGAGAGGAACTTCCAAA	2458
Qy	1681	GATGAGAGGGGACAGGGCCAGCCAGAGGGGACCCCAAGTCCAGAGTGA	1728
Dp	2459	GATGAGAGGGGACAGGGCCAGCCAGAGGGGACCCCAAGTCCAGAGTGA	2506

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; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO000663
; CURRENT APPLICATION NUMBER: US/09/735,932
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Human
US-09-735-932-1

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Query Match	99.6%;	Score 1721.6;	DB 9;	Length 1755;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1724; Conservative	0;	Mismatches	4;	Indels 0; Gaps 0.

QY	1	ATGAGCCAGGACACCAAGTGAACAACAAGATCGAGTCCCGGACCCCATTCGAAGCC	60
Dp	11	ATGAGCCAGGACACCAAGTGAACAACAAGATCGAGTCCCGGACCCCATTCGAAGCC	70
QY	61	AGGAAGTTGCTGCTGCTGTCTGAGCCCATCTGGGATTACTACTGCTGGCTGAACA	120
Dp	71	AGGAAGTTGCTGCTGCTGTCTGAGCCCATCTGGGATTACTACTGCTGGCTGAACA	130
QY	121	ATGGCTTCCAGATCATGATATTAACCTATCATCTCTGGTGCAGAGCCGTGTTCCCGAC	180
Dp	131	ATGGCTTCCAGATCATGATATTAACCTATCATCTCTGGTGCAGAGCCGTGTTCCCGAC	190
QY	181	TTGAGACACGGTTATCTGATGGCCGTGGTGGTGTGACTACAGAGATGACCTGCTATAC	240
Dp	191	TTGAGACACGGTTATCTGATGGCCGTGGTGGTGTGACTACAGAGATGACCTGCTATAC	250
QY	241	CTACTAGACATGATGGTGTGCGCTTCCACACAGAAATCTTGGAACAGGCAATCTGTGTG	300
Dp	251	CTACTAGACATGATGGTGTGCGCTTCCACACAGAAATCTTGGAACAGGCAATCTGTGTG	310
QY	301	GACAAGGGTAGGATCTGAGATCGCTAGCGTGCACCTGGAATTTCTTGTGGAACCTGGCT	360
Dp	311	GACAAGGGTAGGATCTGAGATCGCTAGCGTGCACCTGGAATTTCTTGTGGAACCTGGCT	370
QY	361	TCCCTGAATGCCACAGATGATGATCTAGCGGCTGGGACCGGACACACCAACCTGAGG	420
Dp	371	TCCCTGAATGCCACAGATGATGATCTAGCGGCTGGGACCGGACACACCAACCTGAGG	430
QY	421	CTGAACCGCTTTCTCGCGCGGCCCGCTCTTGGAGGCTTTCGACCGCACAGAACCCGC	480
Dp	431	CTGAACCGCTTTCTCGCGCGGCCCGCTCTTGGAGGCTTTCGACCGCACAGAACCCGC	490
QY	481	ACACCTTAACCAATATGCTTTGATGGCAAGTGATAGGCTTATCATTTTGTGTATAC	540
Dp	491	ACACCTTAACCAATATGCTTTGATGGCAAGTGATAGGCTTATCATTTTGTGTATAC	550
QY	541	CATTGAACACGCTGACTATATCTTGGACCTATCCCGGATACCTGGGCTTCGGGCTGAGCA	600
Dp	551	CATTGAACACGCTGACTATATCTTGGACCTATCCCGGATACCTGGGCTTCGGGCTGAGCA	610
QY	601	TGGGTATACCCGGACCCCGCGCAGCTGCGCTTTGAGCGCTGGCGCGCACTACTAT	660
Dp	611	TGGGTATACCCGGACCCCGCGCAGCTGCGCTTTGAGCGCTGGCGCGCACTACTAT	670
QY	661	AGCTTTACTTCTTCAACGCTGATCTACTACTACATGAGGCAATACACGCGCGCACGAG	720
Dp	671	AGCTTTACTTCTTCAACGCTGATCTACTACTACATGAGGCAATACACGCGCGCACGAG	730
QY	721	GAAGACAGATACCTCTTCAATGATGGGCGACTTCCGTGGCCGTATGGATTTGCGACCC	780
Dp	731	GAAGACAGATACCTCTTCAATGATGGGCGACTTCCGTGGCCGTATGGATTTGCGACCC	790
QY	781	ATCATGGGTAGCATGAGCTCTGTATCTTACAACATGAAACCTGCAATGGGCTTTCTAC	840
Dp	791	ATCATGGGTAGCATGAGCTCTGTATCTTACAACATGAAACCTGCAATGGGCTTTCTAC	850

QY 841 CCAGATGATGACCTGGTGAAGAGTACATGAGCTGACGACCTCAACCGGAGCTGGAG 900  
DB 851 CCAGATGATGACCTGGTGAAGAGTACATGAGCTGACGACCTCAACCGGAGCTGGAG 910  
QY 901 CGGAGGATTTATGAGTGGTATCAGACCTGAGATCAACAAAGATGATGACGAGGTA 960  
DB 911 CGGAGGATTTATGAGTGGTATCAGACCTGAGATCAACAAAGATGATGACGAGGTA 970  
QY 961 GCCATCTTAAAGCACTTGGCTGAGCGGCTGCGGAGAAAGTGGTGGTCTGTCACCTG 1020  
DB 971 GCCATCTTAAAGCACTTGGCTGAGCGGCTGCGGAGAAAGTGGTGGTCTGTCACCTG 1030  
QY 1021 TCCGCTCTGAGCGGAGGAGATCTTTTCAAGACTGTGAGGCGACCTGCTGAGAGAGCTG 1080  
DB 1031 TCCGCTCTGAGCGGAGGAGATCTTTTCAAGACTGTGAGGCGACCTGCTGAGAGAGCTG 1090  
QY 1081 GTGCTGAAGCTGACCGCCGAGACCTACTCAGCAGGTGATATGATGCGCAAGAGAGAC 1140  
DB 1091 GTGCTGAAGCTGACCGCCGAGACCTACTCAGCAGGTGATATGATGCGCAAGAGAGAC 1150  
QY 1141 ATTGGCCAGAGATGATATCATATCCGAGAGGCTCAACTGCGCTGGTGGAGATGATGCT 1200  
DB 1151 ATTGGCCAGAGATGATATCATATCCGAGAGGCTCAACTGCGCTGGTGGAGATGATGCT 1210  
QY 1201 ATCAACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
DB 1211 ATCAACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270  
QY 1261 ATCAAGGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
DB 1271 ATCAAGGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1330  
QY 1321 GACCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
DB 1331 GACCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1390  
QY 1381 CAGACCATCATGAGGAGGAGAAAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
DB 1391 CAGACCATCATGAGGAGGAGAAAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1450  
QY 1441 AATCTGAGGAGCTGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
DB 1451 AATCTGAGGAGCTGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1510  
QY 1501 GACCAAGAGCTGATGATCTACAGACCAAGTTTGTCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 1511 GACCAAGAGCTGATGATCTACAGACCAAGTTTGTCTGCTGCTGCTGCTGCTGCTGCT 1570  
QY 1561 AGGCACTTAAGATGCTTACCGCATGGAAGGCTGAGTGGGCAAGCTCGAGATGGGCA 1620  
DB 1571 AGGCACTTAAGATGCTTACCGCATGGAAGGCTGAGTGGGCAAGCTCGAGATGGGCA 1630  
QY 1621 ATGCCCGAGAGCTGCTGAGGCTGATGACGAGGCTGAGGCTGAGGAGGAACTTCCAAA 1680  
DB 1631 ATGCCCGAGAGCTGCTGAGGCTGATGACGAGGCTGAGGCTGAGGAGGAACTTCCAAA 1690  
QY 1681 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1728  
DB 1691 GATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1738

## RESULT 9

US-10-207-951-1  
; Sequence 1, Application US/10207951  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: Karl GIBLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS  
; FILE REFERENCE: C100063CON  
; CURRENT APPLICATION NUMBER: US/10/207,951

CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1758  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(1758)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-207-951-1  
Query Match 99.6%; Score 1721.6; DB 15; Length 1758;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1724; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ATGAGCCAGAGACACCAAGTGAAGACACAGAGTCCAGTCCCGACGCCATCCAAAGGC 60  
DB 11 ATGAGCCAGAGACACCAAGTGAAGACACAGAGTCCCGACGCCATCCAAAGGC 70  
QY 61 AGAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 71 AGAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130  
QY 121 ATGCTCTTCCAGTATGATATTAACCTCATATCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
DB 131 ATGCTCTTCCAGTATGATATTAACCTCATATCTGCTGCTGCTGCTGCTGCTGCTGCT 190  
QY 181 TTGAGACAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 191 TTGAGACAGGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250  
QY 241 CTACTAGACATGAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 251 CTACTAGACATGAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310  
QY 301 GACAAAGGATGAGATCTGAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 311 GACAAAGGATGAGATCTGAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370  
QY 361 TCCCTGATGCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 371 TCCCTGATGCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430  
QY 421 CTGAACGCTTTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
DB 431 CTGAACGCTTTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 490  
QY 481 ACACTTACCCAAATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 491 ACACTTACCCAAATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
QY 541 CATTGGAACAGCTGCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 551 CATTGGAACAGCTGCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610  
QY 601 TGGGTATACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB 611 TGGGTATACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 670  
QY 661 AGCTTTTACTTCTCAAGCTGATATCTAAGTGGGAGTATACAGCGCGCGCTACCTAT 720  
DB 671 AGCTTTTACTTCTCAAGCTGATATCTAAGTGGGAGTATACAGCGCGCGCTACCTAT 730  
QY 721 GAAGAAGATACCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 731 GAAGAAGATACCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790





178 GACTTGCAGCAGGTTATCTGTGGCTGTGTGCTGGACTACAGAGTGCACCTGTA 237  
Db GACTTGCAGCAGGTTATCTGTGGCTGTGTGCTGGACTACAGAGTGCACCTGTA 293  
QY TACCTACTAGACATGAGTGTGCTGTGCACACA--GGAATCTTGGAAACAGGACATCTG 294  
Db TACCTACTAGACATGAGTGTGCTGTGCACACAAGGTGATCTTGGAAACAGGACATCTG 353  
QY GTGTGACAAAGGTTAGATCTCGAGTCGTACGTTGACCTGGAGTTCTTCTTGAC 354  
Db GTGTGACAAAGGTTAGATCTCGAGTCGTACGTTGACCTGGAGTTCTTCTTGAC 413  
QY CTGGCTTCCCGATGCCCCAGATGTGTGTACGTTGAGGCTGGGGCCGACACACCAACC 414  
Db CTGGCTTCCCGATGCCCCAGATGTGTGTGTACGTTGAGGCTGGGGCCGACACACCAACC 473  
QY CTGAGGCTGAAACCGCTTCTCCGCGCGCCCGCTCTTTCGAGGCTTTCGACCGACAGAG 474  
Db CTGAGGCTGAAACCGCTTCTCCGCGCGCCCGCTCTTTCGAGGCTTTCGACCGACAGAG 533  
QY ACCCGACAGCTTACCCAAATGCTTTCGCACTTGCAGAGCTGATGCTTAACTTTTGTCT 534  
Db ACCCGACAGCTTACCCAAATGCTTTCGCACTTGCAGAGCTGATGCTTAACTTTTGTCT 593  
QY GTCAATCATTTGAAACAGCTGCTTACTTGTGCTTACCTCCGCTTACCTGGGCTTGGGGCT 594  
Db GTCAATCATTTGAAACAGCTGCTTACTTGTGCTTACCTCCGCTTACCTGGGCTTGGGGCT 653  
QY GAGCCATGAGTGTATCCCGGACCCCGCGAGCTGTGAGCGCTGCGGCGCAGTAC 654  
Db GAGCCATGAGTGTATCCCGGACCCCGCGAGCTGTGAGCGCTTGAAGCGCTGCGGCGCAGTAC 713  
QY CTCTATAGCTTTTACTTCTTCCAGCTGTACTGACTACAGTGGGAGTACACCGCCGCA 714  
Db CTCTATAGCTTTTACTTCTTCCAGCTGTACTGACTACAGTGGGAGTACACCGCCGCA 773  
QY GCGAGGGAAGAAAGTACTCTTTCATGAGTGGGCGACTTCCGCTGGGCGCTATGGGTTTC 774  
Db GCGAGGGAAGAAAGTACTCTTTCATGAGTGGGCGACTTCCGCTGGGCGCTATGGGTTTC 833  
QY GCGACCATCATGAGTGTAGAGTGTGTCTGTCTATCTACAAATGAAACATGACAGATCGGCT 834  
Db GCGACCATCATGAGTGTAGAGTGTGTCTGTCTATCTACAAATGAAACATGACAGATCGGCT 893  
QY TTCTAACCAATCATGCACTGTGTGAAGATGATGAACTGTGACAGAGTCAACCGCAAG 894  
Db TTCTAACCAATCATGCACTGTGTGAAGATGATGAACTGTGACAGAGTCAACCGCAAG 953  
QY CTGGAGGCGGAGTATGATGCTGTGTAGACACCTGCGAGATCAACAAAGATGACCAAG 954  
Db CTGGAGGCGGAGTATGATGCTGTGTGTAGACACCTGCGAGATCAACAAAGATGACCAAG 1013  
QY GAGGTAGGCACTTACAGCACTTGTGAGCGGCTGCGGCGAGAAAGTGTGTGTGTG 1014  
Db GAGGTAGGCACTTACAGCACTTGTGAGCGGCTGCGGCGAGAAAGTGTGTGTGTG 1073  
QY CACTGTCTCACTCTGAGCGGCTGTGAATCTTTTCAAGAACTGTGAAGCGCAAGCTGTGAG 1074  
Db CACTGTCTCACTCTGAGCGGCTGTGAATCTTTTCAAGAACTGTGAAGCGCAAGCTGTGAG 1133  
QY GAGCTGTGCTGAGAGCTGAGCGGCGGAGCTACTACAGAGGTAATATGTATGCGCGCAA 1134  
Db GAGCTGTGCTGAGAGCTGAGCGGCGGAGCTACTACAGAGGTAATATGTATGCGCGCAA 1193  
QY GAGACATTTGGCGCAAGATGTATCATCCGAGAGGTTCACTGCGCGTGTGTGACAT 1194  
Db GAGACATTTGGCGCAAGATGTATCATCCGAGAGGTTCACTGCGCGTGTGTGACAT 1253  
QY GATGTATCAACAGTATGCTGTGTCTCGGTGACAGGCTCTACTTTGGGGAATCAGCATC 1254  
Db GATGTATCAACAGTATGCTGTGTCTCGGTGACAGGCTCTACTTTGGGGAATCAGCATC 1313

QY ATCAACATCAAA--GGGAAATGTCTGGAAACCGCGCACAGCCAAATCATGAGCCTTA 1311  
Db ATCAACATCAAAAGTGTGGAAATGTCTGGAAACCGCGCACAGCCAAATCATGAGCCTTA 1373  
QY GGTATTTCAGACCTATTCTGTCTGAGCAGAGGACCTGCGGAGAGTGTGAGCGAGTAT 1371  
Db GGTATTTCAGACCTATTCTGTCTGAGCAGAGGACCTGCGGAGAGTGTGAGCGAGTAT 1433  
QY CCACAAACAGACAGACATCATGAGAGAGAAAGAGAGTGTATCCCTGAAATGAAACAG 1431  
Db CCACAAAGACAGACATCATGAGAGAGAAAGAGAGTGTATCTGTGAAATGAAACAG 1493  
QY TTGACGTGATGTGTGAGGCGAGCTGATGATGCTCCGACAGAGGCGCAGAGATCCGCTA 1491  
Db TTGACGTGATGTGTGAGGCGAGCTGATGATGCTCCGACAGAGGCGCAGAGATCCGCTA 1553  
QY GAGGCTTACAGCAGCAGCTGATGATCTACAGACCAAGTTTGTCTGCTGCTGCTGAG 1551  
Db GAGGCTTACAGCAGCAGCTGATGATCTACAGACCAAGTTTGTCTGCTGCTGCTGAG 1613  
QY CTGAGATCCAGCGGACCTTAAGATGCTTACCGCATTTGAACGCGGTGAGTGCAGACTGA 1611  
Db CTGAGATCCAGCGGACCTTAAGATGCTTACCGCATTTGAACGCGGTGAGTGCAGACTGA 1673  
QY GAGTGCCTAATGCTCCGAGGACCTGCTGAGCTGATGACGAGGTGAGCTGAGAGGGA 1671  
Db GAGTGCCTAATGCTCCGAGGACCTGCTGAGCTGATGATGACGAGGTGAGCTGAGAGGGA 1733  
QY ACTTCCAAAGATGAAAGAGGCGGCGCAACCGAGAGGACCCCGAGGTCCAGAGTGA 1728  
Db ACTTCCAAAGATGAAAGAGGCGGCGCAACCGAGAGGACCCCGAGGTCCAGAGTGA 1790

## RESULT 11

US-10-174-333-27  
Sequence 27, Application US/10174333  
Publication No. US20040029220A1

## GENERAL INFORMATION:

APPLICANT: Vernet, Corine A.M.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Zernhusen, Bryan D.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Majumder, Komud  
APPLICANT: Tchiernev, Velizar T.  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Paturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Gambolli, Esna A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Kasteili, Luca  
APPLICANT: MacDougall, John R.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Grose, William M.  
APPLICANT: Szekeres, Edward S.  
APPLICANT: Alsobrook, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Li, Li  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-783 CIP1  
CURRENT FILING DATE: 2002-06-18  
PRIOR APPLICATION NUMBER: 60/193,664  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 60/194,614  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: 60/195,063  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/195,066



RESULT 12  
US-09-735-932-3  
; Sequence 3, Application US/09735932  
; Patent No. US20020037548A1  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000663  
; CURRENT APPLICATION NUMBER: US/09/735,932  
; CURRENT FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 10989  
; TYPE: DNA  
; ORGANISM: Human  
US-09-735-932-3

Query Match 37.8%; Score 652.6; DB 9; Length 10989;  
Best Local Similarity 99.4%; Pred. No. 1.4e-190;  
Matches 655; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 261 CTTCCACACAGAGATTCTTGAACAGAGGATCTGTGTGACAAAGGTAGATCTGAG 320  
DB 3848 CTTCTCCCAAGAGATTCTTGAACAGAGGATCTGTGTGACAAAGGTAGATCTGAG 3907  
QY 321 TCGCTACGTTGACCTGAGATTCTTGTGACCTGTGCTTCCCTGATGCCACAGATGT 380  
DB 3908 TCGCTACGTTGACCTGAGATTCTTGTGACCTGTGCTTCCCTGATGCCACAGATGT 3967  
QY 381 GGTCTAGGTGGGTGGGCGCCGACACACCACTGTGAGGCTGAACCGCTTTCGCCGC 440  
DB 3968 GGTCTAGGTGGGTGGGCGCCGACACCACTGTGAGGCTGAACCGCTTTCGCCGC 4027  
QY 441 GCCCGCCTCTTCGAGGCTTTCGACCGACAGAGCCGACAGCTTACCCAAATGCTT 500  
DB 4028 GCCCGCCTCTTCGAGGCTTTCGACCGACAGAGCCGACAGCTTACCCAAATGCTT 4087  
QY 501 TCGCATGCCAAGCTGATGCTTTACATTTTGTGTCATCCATTGGAACAGCTGCTATA 560  
DB 4088 TCGCATGCCAAGCTGATGCTTTACATTTTGTGTCATCCATTGGAACAGCTGCTATA 4147  
QY 561 CTTTGCCCTATCCCGGTACCTGGGCTTGGGCGTGAACGATGGGTACCCGGACCCGC 620  
DB 4148 CTTTGCCCTATCCCGGTACCTGGGCTTGGGCGTGAACGATGGGTACCCGGACCCGC 4207  
QY 621 GCAGCTGGCTTTGAGCGCTGCGGCGCAGTACCTCTATAGCTTTTACTTCCACGCT 680  
DB 4208 GCAGCTGGCTTTGAGCGCTGCGGCGCAGTACCTCTATAGCTTTTACTTCCACGCT 4267  
QY 681 GATATGACTACAGTGGGCGATACACCGCGCAGCCAGGGAAGAAGTACCTTTTAT 740  
DB 4268 GATATGACTACAGTGGGCGATACACCGCGCAGCCAGGGAAGAAGTACCTTTTAT 4327  
QY 741 GGTGGGCGACTTCTCGTGGCGCGTATGGGTTTGGCCACCATTCATGGGTAGATGAGTTC 800  
DB 4328 GGTGGGCGACTTCTCGTGGCGCGTATGGGTTTGGCCACCATTCATGGGTAGATGAGTTC 4387  
QY 801 TGTGATCTACAACATGAACACTGACGATGCGGCTTTTCTACCAAGTACATGACTGTGAA 860  
DB 4388 TGTGATCTACAACATGAACACTGACGATGCGGCTTTTCTACCAAGTACATGACTGTGAA 4447  
QY 861 GAAGTACATGAAGCTGACGACGTCACCGCAAGCTGAGGCGGAGTTATTGACTGTT 919  
DB 4448 GAAGTACATGAAGCTGACGACGTCACCGCAAGCTGAGGCGGAGTTATTGACTGTT 4506

RESULT 13  
US-10-207-951-3  
; Sequence 3, Application US/10207951  
; Publication No. US2003013156A1

GENERAL INFORMATION:  
; APPLICANT: Karl GUEGLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000663CON  
; CURRENT APPLICATION NUMBER: US/10/207,951  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 10989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-207-951-3

Query Match 37.8%; Score 652.6; DB 15; Length 10989;  
Best Local Similarity 99.4%; Pred. No. 1.4e-190;  
Matches 655; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 261 CTTCCACACAGAGATTCTTGAACAGAGGATCTGTGTGACAAAGGTAGATCTGAG 320  
DB 3848 CTTCTCCCAAGAGATTCTTGAACAGAGGATCTGTGTGACAAAGGTAGATCTGAG 3907  
QY 321 TCGCTACGTTGACCTGAGATTCTTGTGACCTGTGCTTCCCTGATGCCACAGATGT 380  
DB 3908 TCGCTACGTTGACCTGAGATTCTTGTGACCTGTGCTTCCCTGATGCCACAGATGT 3967  
QY 381 GGTCTAGGTGGGTGGGCGCCGACACACCACTGTGAGGCTGAACCGCTTTCGCCGC 440  
DB 3968 GGTCTAGGTGGGTGGGCGCCGACACCACTGTGAGGCTGAACCGCTTTCGCCGC 4027  
QY 441 GCCCGCCTCTTCGAGGCTTTCGACCGACAGAGCCGACAGCTTACCCAAATGCTT 500  
DB 4028 GCCCGCCTCTTCGAGGCTTTCGACCGACAGAGCCGACAGCTTACCCAAATGCTT 4087  
QY 501 TCGCATGCCAAGCTGATGCTTTACATTTTGTGTCATCCATTGGAACAGCTGCTATA 560  
DB 4088 TCGCATGCCAAGCTGATGCTTTACATTTTGTGTCATCCATTGGAACAGCTGCTATA 4147  
QY 561 CTTTGCCCTATCCCGGTACCTGGGCTTGGGCGTGAACGATGGGTACCCGGACCCGC 620  
DB 4148 CTTTGCCCTATCCCGGTACCTGGGCTTGGGCGTGAACGATGGGTACCCGGACCCGC 4207  
QY 621 GCAGCTGGCTTTGAGCGCTGCGGCGCAGTACCTCTATAGCTTTTACTTCCACGCT 680  
DB 4208 GCAGCTGGCTTTGAGCGCTGCGGCGCAGTACCTCTATAGCTTTTACTTCCACGCT 4267  
QY 681 GATATGACTACAGTGGGCGATACACCGCGCAGCCAGGGAAGAAGTACCTTTTAT 740  
DB 4268 GATATGACTACAGTGGGCGATACACCGCGCAGCCAGGGAAGAAGTACCTTTTAT 4327  
QY 741 GGTGGGCGACTTCTCGTGGCGCGTATGGGTTTGGCCACCATTCATGGGTAGATGAGTTC 800  
DB 4328 GGTGGGCGACTTCTCGTGGCGCGTATGGGTTTGGCCACCATTCATGGGTAGATGAGTTC 4387  
QY 801 TGTGATCTACAACATGAACACTGACGATGCGGCTTTTCTACCAAGTACATGACTGTGAA 860  
DB 4388 TGTGATCTACAACATGAACACTGACGATGCGGCTTTTCTACCAAGTACATGACTGTGAA 4447  
QY 861 GAAGTACATGAAGCTGACGACGTCACCGCAAGCTGAGGCGGAGTTATTGACTGTT 919  
DB 4448 GAAGTACATGAAGCTGACGACGTCACCGCAAGCTGAGGCGGAGTTATTGACTGTT 4506

RESULT 14  
US-10-345-680-27  
; Sequence 27, Application US/10345680  
; Publication No. US20030148394A1





QY 1501 GACCAGCACTGATGATCTACAGACCAAGTTTGCTGCTCTGAGCTGAGNCC 1560  
Db 1939 GGGTCTCTCCCTGAGACCCCTGACAGACCGTTTGCACGCTCTGCTGAGTACACGCC 1998  
QY 1561 AGCGCACTTAAGATTGCTTACCGCATGAGGCTGAGTGGCAG 1605  
Db 1999 ACCCAGATGAAGATGAAGCAGCGTCTCAGCCCACTGGAAGCCAG 2043

Search completed: September 11, 2004, 01:12:28  
Job time : 809.203 secs

Column

Sheet



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 10, 2004, 20:24:05 ; Search time 104 Seconds

(without alignments)  
285.432 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDTKVKTTSSPPAPSKA.....EGTSKDEGRASCPGPGPE 575

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	51.1	690	4	US-09-275-252A-19
2	847	28.3	261	4	US-09-275-252A-18
3	488	16.3	129	4	US-08-997-685A-46
4	475.5	15.9	126	4	US-08-997-685A-57
5	468.5	15.7	126	4	US-08-997-685A-58
6	466.5	15.6	528	4	US-08-997-685A-4
7	450.5	15.1	597	4	US-08-997-685A-12
8	441.5	14.8	749	4	US-08-997-685A-10
9	441.5	14.8	910	4	US-08-997-685A-2
10	420.5	14.1	506	4	US-08-997-685A-6
11	406	13.6	170	4	US-09-358-383C-27
12	402	13.4	319	4	US-09-358-383C-22
13	391	13.1	962	4	US-09-614-480-9
14	391	13.1	962	4	US-09-694-777A-3
15	387.5	13.0	960	4	US-09-694-777A-21
16	387.5	13.0	962	4	US-09-694-777A-24
17	382.5	12.8	1284	4	US-09-343-494-9
18	382.5	12.8	1284	4	US-09-358-383C-11
19	380.5	12.7	989	4	US-09-694-777A-4
20	380	12.7	1083	4	US-09-600-776-2
21	380	12.7	1083	4	US-09-343-494-1
22	379	12.7	1083	4	US-09-358-383C-2
23	377	12.6	987	4	US-09-694-777A-22
24	377	12.6	989	4	US-09-694-777A-23
25	377	12.6	1082	4	US-09-336-643A-20
26	376.5	12.6	988	4	US-09-614-480-2
27	376.5	12.6	988	4	US-10-162-012-5

28	376.5	12.6	1107	4	US-09-358-383C-16	Sequence 16, Appl
29	375	12.5	1159	2	US-08-956-242-13	Sequence 13, Appl
30	375	12.5	1159	3	US-09-351-215-13	Sequence 13, Appl
31	375	12.5	1159	3	US-09-226-012-2	Sequence 2, Appl
32	375	12.5	1159	3	US-09-226-012-4	Sequence 4, Appl
33	375	12.5	1159	3	US-09-358-383C-10	Sequence 10, Appl
34	375	12.5	1159	4	US-09-275-252A-12	Sequence 12, Appl
35	370.5	12.4	888	2	US-08-956-242-4	Sequence 4, Appl
36	370.5	12.4	888	3	US-09-351-215-4	Sequence 12, Appl
37	370	12.4	988	4	US-10-162-012-12	Sequence 12, Appl
38	370	12.4	1102	4	US-09-358-383C-36	Sequence 36, Appl
39	361	12.1	1017	4	US-09-600-776-6	Sequence 6, Appl
40	307.5	10.3	189	4	US-09-358-383C-25	Sequence 25, Appl
41	268.5	9.0	857	4	US-09-275-252A-11	Sequence 11, Appl
42	256.5	8.6	597	4	US-09-275-252A-7	Sequence 7, Appl
43	234	7.8	542	4	US-09-358-383C-5	Sequence 5, Appl
44	225.5	7.5	626	3	US-08-956-242-2	Sequence 2, Appl
45	225.5	7.5	626	3	US-09-351-215-2	Sequence 2, Appl

## ALIGNMENTS

```
RESULT 1
US-09-275-252A-19
; Sequence 19, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderrick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-19
Query Match 51.1%; Score 1526.5; DB 4; Length 690;
Best Local Similarity 53.8%; Pred. No. 1.8e-145;
Matches 284; Conservative 112; Mismatches 131; Indels 1; Gaps 1;
6 KVKTTSSPPAPSKARKLLPYLDSSGDYVYVWNTWVFPVYNTLITVCACFPDLQHG 65
137 KKKKEKSKDKKHKKEVVVIDPSGNTYVWMLFCITLPVYVWNTWVIAKCFDELQSDY 196
197 LEVWLLIDYSDIYLLIDMFVTRTGYLQGLAVKEIKLNNKKSNNLOFLDVLISLPT 256
126 DVVAVRGLGPHPTLRNLNRLAPRLFEAFDTEFRTVYVNAFRJAKMLYFVVIHWNSC 185
257 DLIFKLGKNTPELRNLRLRFSKMFEPQTEFRTVYVNAFRJAKMLYFVVIHWNSC 316
186 LYPALSRVIGRGDAWYVDPDAPGPERLRQYLYSPFSTLLITVGDTPPAREEYL 245
317 VFYSISAKIGKGNLTWYVDPDINDEPGLAKYVYSWSTLTTLTGETPPVDRDSRYV 376
246 FMVGDPLLAWGEATINGSMSVYVYNNVTADAAFYPDHALYKKYMKQHVYRKLERVID 305
377 FVVVDFLIGVIFATVIGNISGMISNNMAARFAERQARIIDAIKQYMHFRVNSKDKERVIK 436
```

QY 306 WYOHQINKMTNEVAILQHLPERLARAVAVSHLSTSRVOIFPNCBASLIEEVLKQ 365  
Db 437 WFDYLMNKKTVDDEKVEKYLPPDKRAEIAINVLHDLTKKVFIFDCEAGLLVELVLQ 496  
QY 366 PQTSPGEYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGEISINIKGM 425  
Db 497 PQTSPGEYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGEISINIKGM 556  
QY 426 SGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMKLDVNAEA 485  
Db 557 AGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMKLDVNAEA 616  
QY 486 EIALQEAESRLRGDQDLQOTKARLAEBSAKIARIRLE 533  
Db 617 GSDPKD-LEEKVTMEGSDVLDQTRFARILAEBSMOCKLQKRLTKE 663

## RESULT 2

US-09-275-252A-18  
; Sequence 18, Application US/09275252A  
; Patent No. 6641997  
; GENERAL INFORMATION:  
; APPLICANT: MacKinnon, Roderick  
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With  
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation  
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof  
; FILE REFERENCE: 018512-002901US  
; CURRENT FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US/09/045,529  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: US 09/054,347  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-275-252A-18

Query Match 28.3%; Score 847; DB 4; Length 261;  
Best Local Similarity 59.8%; Pred. No. 2.7e-77;  
Matches 156; Conservative 52; Mismatches 53; Indels 0; Gaps 0;

QY 186 LYFALSRVLGFGRDAMVYPDPAQPPFRLRQYLYSFSTLILTTVGDTPPPARREYYL 245  
Db 1 IYLAISKIGFVDTWVYFNITDPHYGLAREYICLYLSTLITTTETPPVXDEYLL 60  
QY 246 FMVGDPELLAVNGFATIMGSMSSVYNNMTADAAFPYDHALYKTKLQHVNRKLEERYID 305  
Db 61 FVIDFELGLVILFATIVNGSMISNMNATRAEFQAKIDAVHYVQFVKSGMEAKYIR 120  
QY 306 MYCHLQINKMTNEVAILQHLPERLARAVAVSHLSTSRVOIFPNCBASLIEEVLKQ 365  
Db 121 WFDYLMNKKTVDDEKVEKYLPPDKRAEIAINVLHDLTKKVFIFDCEAGLLVELVLQ 180  
QY 366 PQTSPGEYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGEISINIKGM 425  
Db 181 PQTSPGEYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGEISINIKGM 556  
QY 426 SGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMKLDVNAEA 485  
Db 241 MGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMKLDVNAEA 616

RESULT 3  
US-08-997-685A-46  
; Sequence 46, Application US/0897685A

; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: rat;  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (48)..(49)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (121)..(122)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (125)..(126)  
; OTHER INFORMATION: gap in alignment  
US-08-997-685A-46

Query Match 16.3%; Score 488; DB 4; Length 129;  
Best Local Similarity 71.3%; Pred. No. 2.1e-41;  
Matches 92; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

QY 356 LLEBVLKLOPQTSPEGYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGE 415  
Db 1 LLEBVLKLOPQTSPEGYVCRKGDIGQEMTIREGOLAVVADGDTGYAVLAGALYGE 60  
QY 416 ISIINIKSGMGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMK 475  
Db 61 ISIINIKSGMGNRRANIKSLGYSDFCLSKEDIREVLSPEYPOQOTMEKREILKMK 120  
QY 476 NKLDVNAEA 484  
Db 121 GLDENEVA 129

RESULT 4  
US-08-997-685A-57  
; Sequence 57, Application US/0897685A  
; Patent No. 6551821

; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: bovine;  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (47)..(48)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (56)..(57)  
; OTHER INFORMATION: gap in alignment  
US-08-997-685A-57

Query Match 15.9%; Score 475.5; DB 4; Length 126;

Best Local Similarity 71.7%; Pred. No. 3,6e-40;  
Matches 91; Conservative 20; Mismatches 15; Indels 1; Gaps 1;  
QY 354 ASLLEELVTLKLPQYSPGSEYVCRKGDIGQEMYYIIRREGQAVVADGDTQYAVLGAAGLYF 413  
DB 1 AGLLVELLTKLRPQYSPGSDYICRKGDIKEMYYIIKEGQAVVADGDTQYFVLSGSGYF 59  
QY 414 GEISLINIKGMSGNRRRTANIKSLGSDLFCLSKEDLREVLSEYPOAQTIMEKREITLL 473  
DB 60 GEISLINIKGMSGNRRRTANIKSLGSDLFCLSKEDLREVLSEYPOAQTIMEKREITLL 119  
QY 474 KMKKLDV 480  
DB 120 KQGLLDI 126  
RESULT 5  
US-08-997-685A-58  
; Sequence 58, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 05/5/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 58  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: catfish;  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (7)..(8)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (47)..(48)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (56)..(57)  
; OTHER INFORMATION: gap in alignment  
; FEATURE:  
; NAME/KEY: NON CONS  
; LOCATION: (66)..(67)  
; OTHER INFORMATION: gap in alignment  
US-08-997-685A-58  
Query Match 15.7%; Score 468.5; DB 4; Length 126;  
Best Local Similarity 71.4%; Pred. No. 1.9e-39;  
Matches 90; Conservative 19; Mismatches 16; Indels 1; Gaps 1;  
QY 354 ASLLEELVTLKLPQYSPGSEYVCRKGDIGQEMYYIIRREGQAVVADGDTQYAVLGAAGLYF 413  
DB 1 AGLLVELLTKLRPQYSPGSDYICRKGDIKEMYYIIKEGQAVVADGDTQYFVLSGSGYF 59  
QY 414 GEISLINIKGMSGNRRRTANIKSLGSDLFCLSKEDLREVLSEYPOAQTIMEKREITLL 473  
DB 60 GEISLINIKGMSGNRRRTANIKSLGSDLFCLSKEDLREVLSEYPOAQTIMEKREITLL 119  
QY 474 KMKKLDV 479  
DB 120 KQGLLDI 125  
RESULT 6  
US-08-997-685A-4  
; Sequence 4, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:

; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 05/5/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 528  
; TYPE: PRT  
; ORGANISM: mouse;  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AAC40125  
; DATABASE ENTRY DATE: 1998-05-29  
; RELEVANT RESIDUES: (1)..(504)  
US-08-997-685A-4  
Query Match 15.6%; Score 466.5; DB 4; Length 528;  
Best Local Similarity 25.3%; Pred. No. 3.4e-38;  
Matches 122; Conservative 109; Mismatches 202; Indels 49; Gaps 12;  
QY 26 VLDSGDIYVWMTNTPVVKYNIILVCRACFPDLQHGIVAVMLVDYSDLYLDMV 85  
DB 27 IHHYSDFRFYWDTMLFMVGNLIIIPVGITF--FKETTPAVTFVNVSDTFPLMDLV 84  
QY VRPHGFL--EQGLVVDKGRISRYRTWSFPLDIASIMPTDYY----- 129  
DB 85 INFRTGIYEDNTEIILDPKIKKKYLRKW--FVDFVSSIVDVIFLVEKGIDSEVYKT 143  
QY 130 ---VRLGPHPTLRLNRLRAPRLFEAFDRTE-----TRTAVPNAFRITAKIMLYFVVIH 181  
DB 144 ARLRIVPFTILSLRLRLIRYHGWEEIFHWIYDLASAMRCLNLSMWLLICH 203  
QY 182 WNSCLYPALSRYLGFGRDPAWYPPDPAQGFERLRQY--LYSF---YFSTLILTTVDDT 235  
DB 204 WDGLQFLVPMLODFPSDCWVSIN-----NMVHMSWSELVSFALFKAMSHMLCIGYRQ 257  
QY 236 PPARREERYLFVWDPLLAVVGFAITGSMSSVYNNMTADAAPFDHALVKKYKQHV 295  
DB 258 APESMTDMLTML--SMVIGATCYAMFGHATALLQSUDSSRRQYQEKYQVQYMSFKL 316  
QY 296 NRKLEERVIVWYQHLQINKKMTNEVALIQLPERLRAVAASVHLSTLSRYQIFONCEAS 355  
DB 317 PADFRQKHIDYEH--RQGKKMSDESDIILGELNGLRREIVNPNCKKVLASMPFANADPN 375  
QY 356 LLEBLVTLKLPQYSPGSEYVCRKGDIGQEMYYIIRREGQAVVADGDTQYAVLGAAGLYGE 415  
DB 376 FVTAMLTCLKREVPQPGDYIIRREGTIGKMYFIHGAVSVLTGK--NKEMKLSGSGYGE 433  
QY 416 ISLINIKGMSGNRRRTANIKSLGSDLFCLSKEDLREVLSEYPOAQTIMEKREITLLKM 475  
DB 434 ICL-----LTRGRRTASVRADYCRILSLSDVNFNEVLEBYPMRRRAFEIVADRLDRI 487  
QY 476 NK 477  
DB 488 GK 489  
RESULT 7  
US-08-997-685A-12  
; Sequence 12, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 05/5/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 12

LENGTH: 597  
 TYPE: PRT  
 ORGANISM: human;  
 PUBLICATION INFORMATION:  
 DATABASE ACCESSION NUMBER: AAC39760  
 DATABASE ENTRY DATE: 1998-05-29  
 RELEVANT RESIDUES: (1)..(597)  
 US-08-997-685A-12

Query Match 15.1%; Score 450.5; DB 4; Length 597;  
 Best Local Similarity 25.1%; Pred. No. 1.7e-36;  
 Matches 124; Conservative 107; Mismatches 209; Indels 55; Gaps 12;

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QY 26 VLDSGDYVWMLTWPFVWVWNLIIIVCRACFPDLOGLVAVMLVLDYSDLLYLMMV 85
DB 57 IHHYSDRFYWDMLIMIMVGNLIIIVGITF--FKDPTAPMIVVNSDTPFLMDLV 114
QY 86 VRFHTGFL--EGLIVVDKGRISRYRTWSFFLDLASMFTDYY-----129
DB 115 LMFRTGIVIEENTTEIIDPEKIKKYLRTW--FVVVFVSSIPVDYIFLVEKGDSEVYKT 173
QY 130 ---VRLGHTPTLRLNRLRAPRLFEAPDRTE---TRTAVPNAFRIAKMLYIFVYIH 181
DB 174 ARAARIYRFTKILSLRLRLSLRLRYTHQWBEIFHMTYDLASAVMRICNLISMMLLCH 233
QY 182 WNSCLYFALSRYLGFGRDAMYPPDPAQPFRLRQVLYSF---YFSTLITTVGDTTP 237
DB 234 WDCGLQFLVPLQDPFRCW---SINGVNHSSSELYFALFKAMSHMLCIGYGAQ 289
QY 238 PARBEELFWVGDPLAVMGFATIMGSMSSVYINNTADAAFYPDHALYKKYMLQHYN 297
DB 290 ESMIDIMLTM--SMIVGATCYAMFVGHATALQSLDSSRRQYQKRYQVQYMSFHKLP 348
QY 298 KLERVIDWYQHLOINKNKTEVALLOHLPRLRAEVAVSHLSTLSVQIFQNCESAL 357
DB 349 DFRQKHIDYEH--RYQGMFDEDSILGELNGPLREIYNFCRKLVAAMPFANADPNFV 407
QY 358 EELVAKLQPTYSPEYVCRKGDIGQEMYIIRREGOLAVADDGIQYAVLGAQYFGEIS 417
DB 408 TMLTKLKEFVQFGDYIIRRESTIGKMYFIQHGVAVSUTKG--NKEMKLDGSGYFGEIC 465
QY 418 IINIKGMSGNRRITANKISLGYSDLPCLSKEDLREVISEYPOAQTIMEE-----K 467
DB 466 L-----LTRGRRTASVADTYCRLYSLVDNNEVLEBYPMRRAFTVAIDRLDRIGK 519
QY 468 GREILLKMKLDVNA 482
DB 520 KNSILLKRVQHDLS 534

```

RESULT 8  
 US-08-997-685A-10  
 Sequence 10, Application US/08997685A  
 Patent No. 6551821  
 GENERAL INFORMATION:  
 APPLICANT: The Trustees of Columbia University  
 APPLICANT: Kandel, Eric  
 TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
 FILE REFERENCE: 0575/54806  
 CURRENT APPLICATION NUMBER: US/08/997,685A  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 10  
 LENGTH: 749  
 TYPE: PRT  
 ORGANISM: human  
 PUBLICATION INFORMATION:  
 DATABASE ACCESSION NUMBER: AAC39759  
 DATABASE ENTRY DATE: 1998-05-29  
 RELEVANT RESIDUES: (1)..(749)  
 US-08-997-685A-10

Query Match 14.8%; Score 441.5; DB 4; Length 749;  
 Best Local Similarity 24.2%; Pred. No. 2.1e-35;  
 Matches 120; Conservative 116; Mismatches 202; Indels 57; Gaps 15;

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QY 26 VLDSGDYVWMLTWPFVWVWNLIIIVCRACFPDLOGLVAVMLVLDYSDLLYLMMV 85
DB 13 IHHYSDRFYWDMLIMIMVGNLIIIVGITF--FTEQTTPTMIIIVNSDTPFLMDLV 70
QY 86 VRFHTGFL--EGLIVVDKGRISRYRTWSFFLDLASMFTDYY-----129
DB 71 LMFRTGIVIEENTTEIIDPEKIKKYLRTW--FVVVFVSSIPVDYIFLVEKGDSEVYKT 129
QY 130 ---VRLGHTPTLRLNRLRAPRLFEAPDRTE---TRTAVPNAFRIAKMLYIFVYIH 178
DB 130 ARAARIYRFTKILSLRLRLSLRLRYTHQWBEIFHMTYDLASAVMRICNLISMMLLCH 186
QY 179 VHHNSCLYFALSRYLGFGRDAMYPPDPAQPFRLRQVLYSF---YFSTLITTVGDTTP 236
DB 187 LCHWDGCLQFLVPLQDPFRCW---SINGVNHSSSELYFALFKAMSHMLCIGYGAQ 244
QY 237 PARBEELFWVGDPLAVMGFATIMGSMSSVYINNTADAAFYPDHALYKKYMLQHYN 296
DB 245 FVMSDLMITML--SMIVGATCYAMFVGHATALQSLDSSRRQYQKRYQVQYMSFHKLP 303
QY 297 KLERVIDWYQHLOINKNKTEVALLOHLPRLRAEVAVSHLSTLSVQIFQNCESAL 356
DB 304 ADMQKHIDYEH--RYQGMFDEDSILGELNGPLREIYNFCRKLVAAMPFANADPNF 362
QY 357 LEEVLAKLQPTYSPEYVCRKGDIGQEMYIIRREGOLAVADDGIQYAVLGAQYFGEI 416
DB 363 VTAMLSKIRFEVQFGDYIIRREGAVGKMYFIQHGVAVSUTKG--SKEMKLDGSGYFGEI 420
QY 417 IINIKGMSGNRRITANKISLGYSDLPCLSKEDLREVISEYPOAQTIMEE-----466
DB 421 CLTF--KG-----KRTASVADTYCRLYSLVDNNEVLEBYPMRRAFTVAIDRLDRIG 474
QY 467 GREILLKMKLDVNA 481
DB 475 KNSILLKRVQHDLS 489

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RESULT 9  
 US-08-997-685A-2  
 Sequence 2, Application US/08997685A  
 Patent No. 6551821  
 GENERAL INFORMATION:  
 APPLICANT: The Trustees of Columbia University  
 APPLICANT: Kandel, Eric  
 TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
 FILE REFERENCE: 0575/54806  
 CURRENT APPLICATION NUMBER: US/08/997,685A  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2  
 LENGTH: 910  
 TYPE: PRT  
 ORGANISM: mouse  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (130)..(148)  
 OTHER INFORMATION: S1  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (164)..(185)  
 OTHER INFORMATION: S2  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (208)..(229)  
 OTHER INFORMATION: S3  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (243)..(271)

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OTHER INFORMATION: S4
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (291)..(313)
OTHER INFORMATION: S5
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (332)..(358)
OTHER INFORMATION: P
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (367)..(387)
OTHER INFORMATION: S6
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (472)..(602)
OTHER INFORMATION: CNB
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC53518
DATABASE ENTRY DATE: 1997-12-27
RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2

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Query Match 14.8% Score 441.5; DB 4; Length 910;
Best Local Similarity 24.2%; Pred. No. 2.9e-35;
Matches 120; Conservative 116; Mismatches 202; Indels 57; Gaps 15;

```

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QY 26 VLDSGDYVWMLNTPVWYNNLIIVCRACFPDLQGYLVAMLVLDYSDLYLDMV 85
DB 123 IHHYSDPRFYWDLMIMVGNLIIIPVGITF--FTEGTTTPMIFVNSDVFLLDLI 180
QY 86 VREHTGFL--EQGILVVDKGRISRRYRTWSFFLDIASLMPTDVVY----- 129
DB 181 MNFTGTGVNEDSSIIIDPKVKKMYLKSWM-FVVDFTSSIVDYIFLVEKMDSEYKT 239
QY 130 ---VRLGPHPTLALNPLRPLRPLF-----EAFDRT-EKRTAYPNAFRIAKMLYIFV 178
DB 240 ARAAIRVRFKILSLRLRLSLIRYIHOMEBIFHMTYDILASAVRIFNLIGMML--L 296
QY 179 VHHNSCLYFALSRYLGFGRDAWYPPDPAQGFRLRQYLYSPY--FSTLILTTVGDP 236
DB 297 LCHWDGCLQFLVPLLDQFPDPCWVSLN--EVMNDSWKQYSYALFKAMSHMLCIGYQA 354
QY 237 PPARBEYLFWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKKYMKLOHVN 296
DB 355 PVMSMDLITML--SMIVGATCYAMFVGHATALLQSLDSRRQYQCKYQVEQYMSFHLKP 413
QY 297 KRLERRVLDWYQHLOINKKMTNEVALLOHLPERLRAEVAVSVMHLSRVOIFONCEASL 356
DB 414 ADPRQKHDIYEH-RYQCKIPEDENLISELNDPLREIIVNFCRKLIVATMPLFANADPNF 472
QY 357 LEEBLVLTLOPQYSPGEYVCRKGDIGQEMYIIRREGOLAVVADDGITOYAVLGAIFYGEI 416
DB 473 VTAMLKSLRPREVQPGDYIIRREGAVGKMWFIQHVAVGVITTKS--SKEMLTGSGYFGEI 530
QY 417 SIINIGMNSGNRRITANIKSLGYSDFCLSKEDLREVLSEYPOAQITMER----- 466
DB 531 CLLT-GG-----RTASVADTYCRLYSLSVDNFMNLEBYPMWRRAFEVVALDRIDRG 584
QY 467 KGREILLKXNKLDVN 481
DB 585 KKSILLQKFKQKLDN 599

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RESULT 10
US-08-997-685A-6
; Sequence 6, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806

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CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 506
TYPE: PRT
ORGANISM: mouse;
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC40126
DATABASE ENTRY DATE: 1998-05-29
RELEVANT RESIDUES: (1)..(506)
US-08-997-685A-6

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Query Match 14.1% Score 420.5; DB 4; Length 506;
Best Local Similarity 25.0%; Pred. No. 1.4e-33;
Matches 112; Conservative 102; Mismatches 189; Indels 45; Gaps 12;

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QY 26 VLDSGDYVWMLNTPVWYNNLIIVCRACFPDLQGYLVAMLVLDYSDLYLDMV 85
DB 76 IHHYSDPRFYWDLMIMVGNLIIIPVGITF--FKDENTTPMIFVNSDVFLLDLI 133
QY 86 VREHTGFL--EQGILVVDKGRISRRYRTWSFFLDIASLMPTDVVY----- 129
DB 134 LNFTGTGVNEDSSIIIDPKVKKMYLKSWM-FVVDFTSSIVDYIFLVEKMDSEYKT 192
QY 130 ---VRLGPHPTLALNPLRPLRPLF-----EAFDRT-EKRTAYPNAFRIAKMLYIFV 181
DB 193 ARAAIRVRFKILSLRLRLSLIRYIHOMEBIFHMTYDILASAVRIFNLIGMML--L 252
QY 182 WNSCLYFALSRYLGFGRDAWYPPDPAQGF--EKLKQYLYSPY--FSTLILTTVGDP 237
DB 253 WDGCLQFLVPLLDQFPDPCWV--SINGVNSWQYSALEFKAMSHMLCIGYQA 308
QY 238 PPARBEYLFWGDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKKYMKLOHVN 297
DB 309 VGMSDVWLITML--SMIVGATCYAMFVGHATALLQSLDSRRQYQCKYQVEQYMSFHLKP 367
QY 298 KRLERRVLDWYQHLOINKKMTNEVALLOHLPERLRAEVAVSVMHLSRVOIFONCEASL 357
DB 368 DTRQKHDIYEH-RYQCKMFEDESIIIGELSEPREIIVNFCRKLIVATMPLFANADPNF 426
QY 358 EBLVLTLOPQYSPGEYVCRKGDIGQEMYIIRREGOLAVVADDGITOYAVLGAIFYGEI 417
DB 427 TSMULTLRPREVQPGDYIIRREGITGKMYFIQHVAVGVITTKG--NKETRLADSGYFGEI 484
QY 418 IINIKGNSGNRRITANIKSLGYSDFCL 445
DB 485 L-----LTRGRRTASVADTYCRLVSL 506

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RESULT 11
US-09-358-383C-27
; Sequence 27, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: NNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain
US-09-358-383C-27

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Query Match 13.6%; Score 406; DB 4; Length 170;  
 Best Local Similarity 45.6%; Pred. No. 6.7e-33;  
 Matches 77; Conservative 38; Mismatches 48; Indels 6; Gaps 2;

181 HNNSCYFALSRLGGRDAMVPPDAQGF-----ERLRQVLYGFSTLITTVG-D-234  
 1 HNNACLYWISKYQGGSDAMVGNKKNHMLSTVDNFGKQYICFYMTSLITLITIGGE-60  
 235 TPPAREEYLFWMGDFLLAVMGFATIMGSSSVIYNNMTADAIFYPDHALVKKYMKLQ-294  
 61 MSPPTTSFEVFEVFPDLVGLIFATLIGNVSMISNMNAARTEFQKMDGVKQYMKYRK-120  
 295 VNRKLRVIDYQHLQINKMNEVAIIQHLPERLRAEVAVSHLSTL-343  
 121 IPKELQKRVIKWFEYIMANQGAVDEEELILELDPKRAELAINIHMDTL-169

## RESULT 12

US-09-358-383C-22  
 ; Sequence 22; Application US/09358383C  
 ; Patent No. 6518398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtiss, Roy A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: NMI-055CP  
 ; CURRENT APPLICATION NUMBER: US/09/358.383C  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: USSN 09/119,855  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Patent Ver. 2.0  
 ; SEQ ID NO 22  
 ; LENGTH: 319  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: domain  
 ; US-09-358-383C-22

Query Match 13.4%; Score 402; DB 4; Length 319;  
 Best Local Similarity 33.7%; Pred. No. 5e-32;  
 Matches 101; Conservative 55; Mismatches 92; Indels 52; Gaps 10;

109 YRTWSEFLDIASLMPDVTYVRLGPHF-----PTLRNRLRRLRFAFRTERT-161  
 1 YLKTWFLDLVLTLPDLIYIFFGSDGSGSLFPLRLNRLRLRVAELFRLKEDT-60  
 162 AYRN-ARPLALMLYIFVIMNSC-----LYFALSRY-----LGFGRDAMVP--DP-206  
 61 AFNYFAIRLILKVCVTLIIHNNACVFDILYILISDYDEAERYGFSTDTWYLANDF-120  
 207 AQP-----GFERLRQVLYSFEYFSTLITTVG-DTPPARREEYLFWMGDFLLAVMG-257  
 121 EEPISMTGIRGSPBLKXQYITSLWSTLITTVGADPAPYTRTEKIFVIFDMLFGVIL-180  
 258 FATIMGSSSVIYNNMTADAIFYPDHALVKKYMKLQHVNRKLRVIDYQHLQINK--K-315  
 181 FAYIIGNTSIVYNNNSRTAEFRTMDAVKEFMKFRKLPKRLQERLAVLYFEYTWNSKSD-240  
 316 MTNEVAIIQHLPERLRAEVAVSHLSTLIRVOIFONCEASLLEBLVLKLPQYPSGEVY-375  
 241 GLDEEEVLEQLPKKRAEL-----STLTLITIGGE-----MSPPTTSFEVY-281

## RESULT 13

US-09-614-480-9  
 ; Sequence 9; Application US/09614480  
 ; Patent No. 6586179  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jegla, Timothy James  
 ; APPLICANT: Liu, Yi  
 ; APPLICANT: ICAGEN, Inc.  
 ; TITLE OF INVENTION: Human Eag2

FILE REFERENCE: 018512-002310US  
 ; CURRENT APPLICATION NUMBER: US/09/614,480  
 ; CURRENT FILING DATE: 2000-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/143,467  
 ; PRIOR FILING DATE: 1999-07-13  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 962  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: human ether a-go-go (Eag) 1 voltage-gated  
 ; OTHER INFORMATION: potassium channel  
 ; US-09-614-480-9

Query Match 13.1%; Score 391; DB 4; Length 962;  
 Best Local Similarity 23.7%; Pred. No. 4.2e-30;  
 Matches 143; Conservative 111; Mismatches 258; Indels 92; Gaps 22;

36 WNTWVFPVWNLIIIVCRACFPDLOHGYLVAMLVLDYTSDDLILDMVYRHHGFL-E-94  
 222 WITLILTF--YALLVPVNSFKTRON--VAMLVDSIVDVFIVDIYVNFHTTGVG-276  
 95 QGILVVDKGRISRYRTWSFPLDASLMPDVTYV-----RIGPHTPLRLNRLRAP-148  
 277 AGEVISPDKLIRNNYKTM-FVIDLISCLPYDINAFENVDEGISLSLSLKVRLRLTG-335  
 149 RLEFAPDRTETRLAYNPAFRIAKMLYIF-VIHNNSCYFALSRYLGFORD-----A-200  
 336 RVARKLDHYIEYGA-----AVLVILVCVFLAHMMACTWYSIGDYEIFEDTKTINNS-390  
 201 WYVP--DPAQP-----GFERLRQVLYSFEYFSTLITTVG-DTPPARREEY-244  
 391 WLYQLANDIGTPYQFNGSGSGKWEKGSKSVISSLFTMTSLTSGFGIARSTDIEX-450  
 245 LEWYGFLLAVMGFATIMGSSSVIYNNMTADAIFYPDHALVKKYMKLQHVNRKLERVT-304  
 451 IFVAIMMIGSLYATIFGVNTTIFQOMVANTNRKHEMLNSVRDLKLYQVPGKLSERV-510  
 305 DWYQHLQINKMNEVAIIQHLPERLRAEVAVSHLSTLSVQIFONCEASLLEBLVYKL-364  
 511 DYIVSTWMSRIGDITKVLQICPDMDRADICVHLNRKVFKEHPARLASDGLALAMEF-570  
 365 QPQYPSGEVYCRKGDIGQEMYIIRREGOLAVVADGDTQYAVLGAQYFGEISITINIKN-424  
 571 QTVHCAPEDLIYHAGESVDSLCFVYSGSLVYIQDEYV--AIIKGDVFGV--FWKE-624  
 425 MSGNRRTANIKSLGSDLFCLSKEDREVLSEYPOQOTIMEKREIILKKN-----476  
 625 ATLAGSCANVALYCDLHVIKRDLQKVEFY--TAFSSFSRNLITVNLKRIYR-681  
 477 KL-DYNAEAP-----IALQENTSR--RGDQOQDDLTQX-510  
 682 KISDVKREEREMRKKNAPLILPPDHEVRLPQRFQCKARLAERG-GRDLDLVE-740  
 511 FARLLAEESGALKIYRIERLEWOTREWP--MPEDIAEADGEPEFGTSKDEBRASOE-569  
 741 KGNVITTEASANHSL--VKASVTVYRSPATPVSFOAASISGVVDH--AKLQARGSECL-795  
 570 GPPG-573  
 796 GPKG-799

## RESULT 14

US-09-694-777A-3  
 ; Sequence 3; Application US/09694777A  
 ; Patent No. 6638736  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
 ; APPLICANT: STUMER, WALTER  
 ; APPLICANT: BECKH, SYNNOVE

; APPLICANT: BRUGEMANN, ANDREA  
 ; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
 ; APPLICANT: PEREZ, ARACELI SANCHEZ  
 ; APPLICANT: WESELOH, RUDIGER  
 ; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
 ; FILE REFERENCE: MPG-8  
 ; CURRENT APPLICATION NUMBER: US/09/694,777A  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
 ; PRIOR FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
 ; PRIOR FILING DATE: 1998-04-21  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 962  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-694-777A-3

Query Match 13.1%; Score 391; DB 4; Length 962;  
 Best Local Similarity 23.7%; Pred. No. 4.2e-30;  
 Matches 143; Conservative 111; Mismatches 256; Indels 92; Gaps 22;

QY 36 MWLNTWPPVYNYLILVCRACFPDQHGVLVAMLVLDYSDLLYLLDMVFRHTGFL-E 94  
 DB 222 WIIILTF---YALIVPVNVSEKTRQNN--VAMLVDSIVDVIIVLIVNFTTGVGP 276  
 QY 95 QGILVVDKGRISRYVWTSFPLDASIMPTDVVVY-----RLGPHPTLRNRFAP 148  
 DB 277 AGEVISDPKLRNMYLKTW-FVIDLISCLPYDVINAFENDEGISLSSLKVRLRLG 335  
 QY 149 RLFEAPDRTRTRAYPAFRIAKMLYIF-VVIHNSCLFALSRYIGFGRD-----A 200  
 DB 336 RVARKLDHYIEYGA-----AVLVILVCVFGIAAHMAACIWSIGDYIFEDTKTIRNS 390  
 QY 201 WVPY---DPAQP-----GFERLRQYLYSFYSTLLITTVG-DTPPARREY 244  
 DB 391 WLQQLAMDIGTPQPNFGSGSGKWEKGSKNVSISSLYFTWSTLSVGFNINAPSTDIEK 450  
 QY 245 LFWAGDFLLAVMGFATIMSGSSVIVNNTADAFYDHALYKVMKLOHVNKLEERYI 304  
 DB 451 IFVAIVMTIGSLIYATIFGNVTITFQOMVANTNRHYHMLNSVRDFKLTVGPXGLSERVM 510  
 QY 305 DWYQHLQIKKMTNEVALIQLPERLRAEVAVSHLSTLSRVOIFONCEASLLEELV 364  
 DB 511 DYIVSTWMSRGIDTEKVIQICPKMRADICVHLNKVFEHHPAFRLASGCLRALAMEF 570  
 QY 365 QPOTYSPGEYVCRKGDIGQEMYIIRREGOLAVVADGITOYAVLAGALYGEISIIINIKG 424  
 DB 571 QTVHCAFGDLIYHAGSVSLCFVVSGLFVIODDDEVV--ALIGKGVFDV----FWKE 624  
 QY 425 MSGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOAQITMEKRGRIILKMN----- 476  
 DB 625 ATLQSCANVRALTYCDLHVIRKDALQKLEFY---TAFSHSFSRNLITLYNLRKRIYVR 681  
 QY 477 KL-DYNAEAE-----IALQEAATESRL-----RGIDQQLDDLQTK 510  
 DB 682 KISDVKREERERMRKNEAPLILPDPHVRRLFORRQCKEARLAALAE--GRHLDLDLVE 740  
 QY 511 PARLAELESSALKIATYERLEEMQTRFMP-MPEDLAEADDEGEPEEGTSKDEGRASGE 569  
 DB 741 KKNVLTHERASNHST---VKASVVTYRESPATPVSPQASTSGVDPH--AKIQAPSSBCL 795  
 QY 570 GPPG 573  
 DB 796 GPKG 799

RESULT 15  
 US-09-694-777A-21  
 ; Sequence 21, Application us/09694777A

; Patent No. 6638736  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
 ; APPLICANT: STUMMER, WALTER  
 ; APPLICANT: BECKH, SYMNOVE  
 ; APPLICANT: BRUGEMANN, ANDREA  
 ; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
 ; APPLICANT: PEREZ, ARACELI SANCHEZ  
 ; APPLICANT: WESELOH, RUDIGER  
 ; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
 ; FILE REFERENCE: MPG-8  
 ; CURRENT APPLICATION NUMBER: US/09/694,777A  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
 ; PRIOR FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
 ; PRIOR FILING DATE: 1998-04-21  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 21  
 ; LENGTH: 960  
 ; TYPE: PRT  
 ; ORGANISM: Bovine sp.  
 US-09-694-777A-21

Query Match 13.0%; Score 387.5; DB 4; Length 960;  
 Best Local Similarity 24.9%; Pred. No. 9.5e-30;  
 Matches 132; Conservative 101; Mismatches 226; Indels 71; Gaps 19;

QY 36 MWLNTWPPVYNYLILVCRACFPDQHGVLVAMLVLDYSDLLYLLDMVFRHTGFL-E 94  
 DB 222 WIIILTF---YALIVPVNVSEKTRQNN--VAMLVDSIVDVIIVLIVNFTTGVGP 276  
 QY 95 QGILVVDKGRISRYVWTSFPLDASIMPTDVVVY-----RLGPHPTLRNRFAP 148  
 DB 277 AGEVISDPKLRNMYLKTW-FVIDLISCLPYDVINAFENDEGISLSSLKVRLRLG 335  
 QY 149 RLFEAPDRTRTRAYPAFRIAKMLYIF-VVIHNSCLFALSRYIGFGRD-----A 200  
 DB 336 RVARKLDHYIEYGA-----AVLVILVCVFGIAAHMAACIWSIGDYIFEDTKTIRNS 390  
 QY 201 WVPY---DPAQP-----GFERLRQYLYSFYSTLLITTVG-DTPPARREY 244  
 DB 391 WLQQLAMDIGTPQPNFGSGSGKWEKGSKNVSISSLYFTWSTLSVGFNINAPSTDIEK 450  
 QY 245 LFWAGDFLLAVMGFATIMSGSSVIVNNTADAFYDHALYKVMKLOHVNKLEERYI 304  
 DB 451 IFVAIVMTIGSLIYATIFGNVTITFQOMVANTNRHYHMLNSVRDFKLTVGPXGLSERVM 510  
 QY 305 DWYQHLQIKKMTNEVALIQLPERLRAEVAVSHLSTLSRVOIFONCEASLLEELV 364  
 DB 511 DYIVSTWMSRGIDTEKVIQICPKMRADICVHLNKVFEHHPAFRLASGCLRALAMEF 570  
 QY 365 QPOTYSPGEYVCRKGDIGQEMYIIRREGOLAVVADGITOYAVLAGALYGEISIIINIKG 424  
 DB 571 QTVHCAFGDLIYHAGSVSLCFVVSGLFVIODDDEVV--ALIGKGVFDV----FWKE 624  
 QY 425 MSGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOAQITMEKRGRIILKMN----- 476  
 DB 625 ATLQSCANVRALTYCDLHVIRKDALQKLEFY---TAFSHSFSRNLITLYNLRKRIYVR 681  
 QY 477 KL-DYNAEAEIALQEAATESRL-----RGIDQQLDDLQTKPARLAE 517  
 DB 682 KISDVKREERERMRKNEAPLILPDPHVRRLFORRQCKEARLAALAE 728

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 Job time : 106 secs

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Sheet



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 11, 2004, 01:12:40 ; Search time 121 Seconds  
(without alignments)  
2637.163 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDTKVKTTBSSPPAPSKA.....EGTSKDEBRASQEGPPGPE 575

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466.5	15.6	1584	US-08-997-685A-3	Sequence 3, Appli
2	441.5	14.8	2263	US-08-997-685A-9	Sequence 9, Appli
3	441.5	14.8	2733	US-08-997-685A-1	Sequence 1, Appli
4	403.5	13.5	1790	US-08-997-685A-11	Sequence 11, Appl
5	400	13.4	3041	US-09-694-777A-20	Sequence 20, Appl
6	399.5	13.4	3041	US-09-694-777A-19	Sequence 19, Appl
7	395.5	13.2	2886	US-09-694-777A-13	Sequence 13, Appl
8	395.5	13.2	3002	US-09-694-777A-1	Sequence 1, Appli
9	389.5	13.0	2967	US-09-614-480-1	Sequence 1, Appli
10	389.5	13.0	2967	US-10-162-012-6	Sequence 6, Appli
11	389.5	13.0	3553	US-10-162-012-4	Sequence 4, Appli
12	385	12.9	2967	US-09-694-777A-14	Sequence 14, Appl

13	385	12.9	3083	4	US-09-694-777A-2	Sequence 2, Appli
14	382.5	12.8	3715	4	US-09-600-776-9	Sequence 9, Appli
15	380	12.7	3249	4	US-09-343-494-2	Sequence 2, Appli
16	380	12.7	3233	4	US-09-600-776-1	Sequence 1, Appli
17	379	12.7	3249	4	US-09-358-383C-3	Sequence 3, Appli
18	379	12.7	3355	4	US-09-358-383C-1	Sequence 1, Appli
19	377	12.6	3857	4	US-09-336-643A-19	Sequence 19, Appl
20	376.5	12.6	3321	4	US-09-358-383C-17	Sequence 17, Appl
21	376.5	12.6	5107	4	US-09-358-383C-15	Sequence 15, Appl
22	375	12.5	3480	3	US-09-226-012-1	Sequence 1, Appli
23	375	12.5	3950	3	US-09-226-012-3	Sequence 3, Appli
24	372.5	12.5	1507	4	US-08-997-685A-5	Sequence 5, Appli
25	370.5	12.4	3142	2	US-08-956-242-3	Sequence 3, Appli
26	370.5	12.4	3142	3	US-09-351-215-3	Sequence 3, Appli
27	362	12.1	3736	4	US-09-600-776-10	Sequence 10, Appl
28	361	12.1	3064	4	US-09-600-776-5	Sequence 5, Appli
29	352.5	11.8	1307	4	US-09-172-422-3	Sequence 3, Appli
30	237.5	7.9	5955	4	US-09-358-383C-14	Sequence 14, Appl
31	234	7.8	1626	4	US-09-358-383C-6	Sequence 6, Appli
32	234	7.8	2694	4	US-09-358-383C-4	Sequence 4, Appli
33	231	7.7	3141	2	US-08-956-242-1	Sequence 1, Appli
34	231	7.7	3141	3	US-09-351-215-1	Sequence 1, Appli
35	219.5	7.3	2173	1	US-08-795-788-1	Sequence 1, Appli
36	219.5	7.3	2173	5	PCT-US93-03942-1	Sequence 1, Appli
37	130.5	4.4	2802	4	US-09-417-197-134	Sequence 134, App
38	129.5	4.3	2799	4	US-09-417-197-136	Sequence 136, App
39	129	4.3	4262	4	US-09-521-511C-10	Sequence 10, Appl
40	128	4.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
41	128	4.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
42	124.5	4.2	453	4	US-09-521-511C-8	Sequence 8, Appli
43	122.5	4.1	2873	4	US-09-669-751-260	Sequence 260, App
44	121.5	4.1	3036	4	US-09-016-434-1155	Sequence 1155, Ap
45	110	3.7	6175	4	US-08-875-435B-1	Sequence 1, Appli

#### ALIGNMENTS

##### RESULT 1

US-08-997-685A-3  
; Sequence 3, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1584  
; TYPE: DNA  
; ORGANISM: mouse;  
US-08-997-685A-3

Alignment Scores:  
Pred. No.: 2.53e-46 Length: 1584  
Score: 466.50 Matches: 122  
Percent Similarity: 47.93% Conservatives: 109  
Best Local Similarity: 25.31% Mismatches: 202  
Query Match: 15.61% Indels: 49  
DB: 4 Gaps: 12

US-09-927-267-1 (1-575) x US-08-997-685A-3 (1-1584)

Qy 26 ValLeuAspProSerGlyAspTyrTyrTrpTrpLeuAsnThrMetValPheProVal 45  
Db 79 ATCATCACCCCTACAGGACTTCTACGGAGCTTCACCTGCTGTGTTGTCATG 138  
Qy 46 MetTyrAsnLeuLeuLeuValCysArgAlaCysPheProAspLeuGlnHisGlyTyr 65  
Db 139 GTGGGAATCTCATATCATTCCTCCGCGGCATCATCTTC-----TTCAAGGACGAGACC 192

QY	66	LeuValAlaTrpLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAspMetVal	85
DB	193	ACCGCGCCCTGGATGCTTCAACGTGGTCTCGGACACTTCTCTCTCATGGACTGGTG	252
QY	86	ValArgPheHisThrGlyPheLeu-----GluGlnGlyLeuValValAspLysGly	103
DB	253	TTGAACCTCCGACCCGGCATTTATTAGAGACAACACGAGACATCTCTGGACCCCGAG	312
QY	104	ArgIleSerSerArgTyrValArgThrTrpSerPhePheLeuAspLeuAlaSerLeuMet	123
DB	313	AAAGTAAAGAAGACTTTCGTACGTGG-----TTCGTGGTGACTTCGTGTCTATCCATC	369
QY	124	ProThrAspValValTyr-----	129
DB	370	CCGGTGGACTACATCTTCCTCATAGTGGAGAGGAATCGACTCCGAGGCTCTACAAGACA	429
QY	130	-----ValArgLeuGlyProHisThrProThrLeuArgLeuAsnArgPheLeuArg	146
DB	430	GC CGCGTCTCTGGGCATCTGCGCGTTCACCAAGATCCTCAGTCTGTGTGGCGTCTGCCG	489
QY	147	AlaProArgLeuPheGluAlaPheAspArgThrGlu-----ThrArgThr	161
DB	490	CTATCAGCGCTCATCCGATATATCCACCACTGGGAGAGATTTTCCACATGACTACGAC	549
QY	162	AlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePheValValIleHis	181
DB	550	CTGGCAAGTCAGTGATCGCATCTGPAACCTGATCAGCATGATGTACTGTCTGCCAC	609
QY	182	TrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGlyPheGlyArgAspAlaTrp	201
DB	610	TGGACCGTTTGCCTCGCATGTTCTGTGCCCATGTGCAAGACTTCCCCACGCACTGCTG	669
QY	202	ValTyrProAspProAlaGlnProGlyPheGluArgLeuArgArgGlnTyr-----Leu	219
DB	670	GTGTCCATCAAC-----AACATGTTGAACCACTCGTGGACGGAGCTC	711
QY	220	TyrSerPhe-----TyrPheSerThrLeuIleLeuThrThrValGlyAspThr	235
DB	712	TACTCGTTGGCGCTCTTCAAGGCCCATGAGCCACATGTGTGCATCGGCTACGGCGGCGAG	771
QY	236	ProProAlaArgGluGluGluTyrLeuPheMetValGlyAspPheLeuLeuAlaVal	255
DB	772	GC GCGCCGAGCATGACAGACATCTGCTGACCATCTCTC---AGCATGTGTAGGCGCC	828
QY	256	MetGlyPheAlaThrIleMetGlySerMetSerSerValIleTyrAsnMetAsnThrAla	275
DB	829	ACCTGCTATGCCATGTTCATTTGGGCACGCCACTGCGCTCATCCAGTCCCTGGATTCGTCA	888
QY	276	AspAlaAlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeuGlnHisVal	295
DB	889	CGGCGCCAATACCAGGAGAGTAGCAACAAGTAGACAAATACATGTCTTCCCAAACTG	948
QY	296	AsnArgLysLeuGluArgArgValIleAspTrpTrpGlnHisLeuGlnIleAsnLysLys	315
DB	949	CCCGCTGACTTCCGCGAGAGACTCCAGATTACTATTGAACAC---CGGTACCAAGGGAAG	1005
QY	316	MetThrAsnGluValAlaIleLeuGlnHisLeuProGluArgLeuArgAlaGluValAla	335
DB	1006	ATGTCCTGATGAGGACAGCATCTTGGGAACTCAACGCGCCACTGCGTGAGGAGATTGTG	1065
QY	336	ValSerValHisLeuSerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSer	355
DB	1066	AACATTCAACTCCGCGAAGCTGTGGCTTCCATGCGCTGTTCACATGACAGACCCCAAT	1125
QY	356	LeuLeuGluGluLeuValLeuLysLeuGlnProGlnThrTyrSerProGlyGluTyrVal	375
DB	1126	TTCGTACAGCATGCTGACAAAGCTCAAAATTGAGGTCTTCCAGCTCGAGATTATCATC	1185
QY	376	CysArgLysGlyAspIleGlyGlnGluMetTyrIleIleArgGluGlyGlnLeuAlaVal	395
DB	1186	ATCCGAGAGGGGACATCCGGAAGAAGATGACTTTCATCCAGCATGGGTTGGTGGAGGTG	1245

Qy	396	ValAlaAspGlyIleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGlu	415
Db	1246	CTCACAAGGCG-----AACACGAGAGATGAACGCTTCGGATGGCTCTATTTCGGGGAG	1299
Qy	416	IleSerIleIleAsnIleLysGlyAsnMetSerGlyAsnArgThrAlaAsnIleLys	435
Db	1300	ATTGCTTG-----CTCAGAGGGCGCGCTACGGCCACGGTCGA	1341
Qy	436	SerLeuGlyTyrSerAspLeuPheCysLeuSerLysGluAspLeuArgGluValLeuSer	455
Db	1342	GCTGACACCTACTGTGGCTCTACTCACTGAGTGTGGACAATTTCACGAGGTCTGGAG	1401
Qy	456	GluTyrProGlnAlaGlnThrIleMetGluGlyLysArgGluIleLeuLeuLysMet	475
Db	1402	GAATACCCCATGATCGCGCGTGCCTTTGACATGTGGCTATTGACCGGGCTAGATCGCAT	1461
Qy	476	AsnLys	477
Db	1462	GGCAAG	1467

## RESULT 2

US-08-997-685A-9  
; Sequence 9, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 2263  
; TYPE: DNA  
; ORGANISM: human  
; US-08-997-685A-9

Alignment Scores:	5.2e-43	Length:	2283
Pred. No.:	441.50	Matches:	120
Score:	41.50	Conservative:	116
Percent Similarity:	47.68%	Mismatches:	202
Best Local Similarity:	24.24%	Indels:	57
Query Match:	14.7%	Gaps:	15
DB:	4		

US-09-927-267-1 (1-575) x US-08-997-685A-9 (1-2263)

Qy	26	VallLeuAspProSerGlyAspTyrTyrTrpTrpLeuAsnThrMetValPheProVal	45
Dd	37	ATTATCACCCCTTACAGTGATTTACGGTTTTACTGGGATTTAAATAATGCTCATATGATG	96
Qy	46	MetTyrAsnLeuIlelleLeuValCysArgAlaCysPheProAspLeuGlnHisGlyTyr	65
Dd	97	GTTGGAAATCTAGTCATCATACCAGTGTGAATTCACATTC-----TTTACAGACAACA	150
Qy	66	LeuValAlaTrpLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAspMetVal	85
Dd	151	ACAACACCATCGATTATTTCAATGTGCATCAGATACAGTTTCTCTATTTGGACCTGAT	210
Qy	86	ValArgPheHisThrGlyPheLeu-----GluGlnGlyIleLeuValValAspLysGly	103
Dd	211	ATGAATTTTAGGACTGGGACTGTCNAATGAAGACAGCTCTGAAATCATCTGGACCCCANA	270
Qy	104	ArgIleSerSerArgTyrValArgThrTrpSerPheLeuAspLeuAlaSerLeuMet	123
Dd	271	GTGATCAAGATCAATTATTTAAAGCTGG---TTTGGTGTGACTTCATCTCATCCATC	327
Qy	124	ProThrAspValValTyr-----	129
Dd	328	CCAGTGGGATATATCTCTTTCTTTATTGTAGAAAAGGAATGGATCTTCAAGTTTACAGACA	387





Db 761 GTG-----TCCATCAATGCGTGTGTAACCACTCGTGGAGTGAACCTGACTCC 808  
Qy 222 Phe-----TyrPheSerThrLeuLeuLeuThrValGlyAspThrProPro 237  
Db 809 TTCGCACTTCAAGGCCATGAGCCACATGCTGTCATCGGGTACGGCGGCGAGCGGCC 868  
Qy 238 ProAlaArgGluGluThrLeuLeuLeuValMetGly 257  
Db 869 GAAAGCATGACGACATCTGGCTGACCATGCTC---AGCATGATTGGTGGCCACCTGC 925  
Qy 258 PheAlaThrIleMetGlySerMetSerValIleTyrAsnMetAsnThrAlaAspAla 277  
Db 926 TACGCCATGTTCTCGGCCACGCCACTGCTCCCTCATCCAGTCTGCTGACTCTCCCGCGGCGC 985  
Qy 278 AlaPheTyrProAspHisAlaLeuValLysTyrMetLysLeuGlnHisValAsnArg 297  
Db 986 CAGTACAGGAGAACTCAAGCAGGTGGAGCATGATGCTCCCAAGCTGCCAGCT 1045  
Qy 298 LysLeuGluArgValIleAspTyrGlnHisLeuGlnIleAsnLysLysMetThr 317  
Db 1046 GACTTCCGCCAGAGATCCACGACTACTATGACAC---CGTACCAGGCGAAGATGTT 1102  
Qy 318 AsnGluValAlaIleLeuGlnHisLeuProGluArgLeuAlaGluValAlaValSer 337  
Db 1103 GACGAGGACATCTCTGGCGAGCTCAACGGGCCCTCGCGGAGAGATCGTCAACTTC 1162  
Qy 338 ValHisLeuSerThrLeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeu 357  
Db 1163 AACTGCCGAGAGCTGGTGGCTTCCATCGCTGTTCGCCAACCGCGACCCCAACTTCGTC 1222  
Qy 358 GluGluLeuValLeuLeuGlnProGlnThrTyrSerProGlyGluTyrValCysArg 377  
Db 1223 ACGGCCATGCTGACCAAGCTCAAGTTCGAGCTCTCCAGCGGGTGACTATCATCTCCG 1282  
Qy 378 LysGlyAspIleGlyGlnGluMetTyrIleLeuArgGluGlyGlnLeuAlaValAla 397  
Db 1283 GAAAGCACCACCTCGGAGAGAGATGACTTCTATCCAGCAGCGCGTGTGAGCGTGTCTACT 1342  
Qy 398 AspAspGlyIleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGluIleSer 417  
Db 1343 AAGGGC-----ACAAGAGATGAAGCTGTCGCGATGCTCTACTTCGGGGAGATCTGC 1396  
Qy 418 IleIleAsnIleLysGlyAsnMetSerGlyAsnArgArgThrAlaAsnIleLysSerLeu 437  
Db 1397 CTG-----CTCACC CGGCGCGCCGCCACGCGGAC-GTCCGGGCTGAC 1437  
Qy 438 GlyTyrSerAspLeuPheCysLeuSerLysGluAspLeuArgGluValLeuSerGluTyr 457  
Db 1438 ACCTACTGCCGCTCTATTCCTCGAGCGTGACAACTTCAACGAAAGTCTGGAGAGTAC 1497  
Qy 458 ProGlnAlaGlnThrIleMetGluGlu-----lys 467  
Db 1498 CCCATGATGGCGCGCTTCGAGAGGTGGCCATCGACCCCTGGACCGCATCGGCAAG 1557  
Qy 468 GlyArgGluLeuLeuLysMetAsnLysLeuAspValAsnAla 482  
Db 1558 AAGAAATCCATCTCTCGCACAGAGTGCAGATGACCTCACTCACTCG 1602

RESULT 5  
US-09-694-777A-20  
; Sequence 20, Application US/09694777A  
; Patent No. 6638736  
; GENERAL INFORMATION:  
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
; APPLICANT: STUMMER, WALTER  
; APPLICANT: BECKH, SYNNOVE  
; APPLICANT: BRUGGMANN, ANDREA  
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
; APPLICANT: PEREZ, ARACELI SANCHEZ  
; APPLICANT: WESELOH, RUDIGER  
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: MPG-8

; CURRENT APPLICATION NUMBER: US/09/694,777A  
; CURRENT FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 3041  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-694-777A-20

Alignment Scores:  
Pred. No.: 9,78e-38 Length: 3041  
Score: 400.00 Matches: 148  
Percent Similarity: 43.85% Conservative: 123  
Best Local Similarity: 23.95% Mismatches: 256  
Query Match: 13.38% Indels: 92  
DB: 4 Gaps: 22

US-09-927-267-1 (1-575) x US-09-694-777A-20 (1-3041)

Qy 11 GluSerSerProProAlaProSerLysAlaArgLysLeuLeuProValLeuAspProSer 30  
Db 625 CAGACATCTCTCCCGAGTACAGCAAGAGCGCCAAAGACACCCCTC-----ACA 675  
Qy 31 GlyAspTyrTyrTyr-----Tyr-----TyrLeuAsnThrMetValPhe 43  
Db 676 TCATCTTACAC-TACTGTGTCTTAAAGACCACATGGGATTGATC-----ATCTGTATC 728  
Qy 44 ProValMetTyrAsnLeuIleLeuValCysArgAlaCysPheProAspLeuGlnHis 63  
Db 729 CTGACCTTCTACACAGCCATCTCTGTCTCTTACACGCTCTCTTAAACACCGAGCAGAAT 788  
Qy 64 GlyTyrLeuValAlaTyrLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAsp 83  
Db 789 AAC-----GTGGCTGGCTGGTGACACATCGTGGATGATCATCTTTTGTGTGGAC 842  
Qy 84 MetValValArgPheHisThrGlyPheLeu---GluGlnGlyIleLeuValValAspLys 102  
Db 843 ATTCTCTGTAATTTTCACACCATCTTGTGGCGGAGGAGGATCTGTGACCC 902  
Qy 103 GlyArgIleSerSerArgTyrValArgThrTrpSerPhePheLeuAspLeuAlaSerLeu 122  
Db 903 AAACCTTATCGCATGAACACTACCTGAAGACGTGG---TTTGTGATCGACCTTCTCTCTGT 959  
Qy 123 MetProThrAspValValTyrVal-----ArgLeuGlyProHisThr 136  
Db 960 TTGCATATGACGTATCAACGCTTTTGAGAACGTGGATGAGGCATCAGCAGCTGTTC 1019  
Qy 137 ProThrLeuArgLeuAsnArgPheLeuAlaProArgLeuPheGluAlaPheAspArg 156  
Db 1020 AGTTCTCTGAAGTGTGGCGGCTCTCGTCTCGAGCAGTGGCGCCCAAGCTGACCAT 1079  
Qy 157 ThrGluThrArgThrAlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIle 176  
Db 1080 TATATCGATGACGAGCGC-----GCGGTACTGTGCTCTGTGTGGTG 1124  
Qy 177 Phe---ValValIleHisTyrAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGly 195  
Db 1125 TTGGGCTGGCTGCCCACTGGATGGCTCATCTGTGTACAGCATTTGGGATTATGATC 1184  
Qy 196 PheGlyArgAsp-----AlaTyrValTyrPro-----Asp 205  
Db 1185 TTTGATGAAGACCAACAGACCATCCGTAACACAGCTGGCTCTACCAACTGGCATTCGAC 1244  
Qy 206 ProAlaGlnPro-----GlyPheGluArg 213  
Db 1245 ATTGGCACTCCATACAGTTTAAATGGTCTGTGTCGGGAAGTGGGAGCGGGCCCAAGC 1304  
Qy 214 LeuArgArgGlnTyrLeuTyrSerPheTyrPheSerThrLeuIleLeuThrValGly 233

Db 1305 AAGAACTCCGATACATTTCTCGTGTACTTCCATGACAAAGTCTCCACAGTGTGGC 1364  
Qy 234 ---AspThrProProAlaArgGluGluTyrLeuPheMetValGlyAspPheLeu 252  
Db 1365 TTTGGTAACATCGCCCATCCACAGATCGAAGATCTTCGCGTAGCCATCATGATG 1424  
Qy 253 LeuAlaValMetGlyPheAlaThrIleMetGlySerMetSerValIleTyrAsnMet 272  
Db 1425 ATTGGCTCCCTTCTGTATGCCACCATCTTTGGGAATGTGACGACCATTTCCAGCAGATG 1484  
Qy 273 AsnThrAlaAspAlaAlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeu 292  
Db 1485 TATGCCAACACCAACAGTATCATGAGATGCTCAACAGCTCCGGATTTCTGAGATC 1544  
Qy 293 GlnHisValAsnArgLysLeuGluArgValIleAspTyrTyrGlnHisLeuGlnIle 312  
Db 1545 TACCAGGTGCCAAGGGCTGAGCGGCTCATGGACTACATTTGTGTACTGTGCTCC 1604  
Qy 313 AsnLysLysMetThrAsnGluValAlaIleLeuGlnHisLeuProGluArgLeuAla 332  
Db 1605 ATGTCCCGCGCATCGACGAGAGGTCTGCAAAATCTGCCCAAGACATGCGAGCT 1664  
Qy 333 GluValAlaValSerValHisLeuSerThrLeuSerArgValGlnIlePheGlnAsnCys 352  
Db 1665 GACATTTGGTACCTGACCGAAGAGTGTCCAAAGAACACCCCGCTTCGGCTGGCC 1724  
Qy 353 GluAlaSerLeuLeuGluLeuValLysLysLeuGlnProGlnThrTyrSerProGly 372  
Db 1725 AGCGATGTTGCTGAGGSCCTTGCCATGGAGTTCACAGACATACATCGCCCCAGGG 1784  
Qy 373 GluTyrValCysArgLysGlyAspIleGlyGlnGluMetTyrIleLeuArgGluGln 392  
Db 1785 GACCTCATCTATCACCGCGGAGAGTGTGGACGCTCTGCTGTGCTCTCGGGCTCC 1844  
Qy 393 LeuAlaValValAlaAspGlyIleThrGlnTyrAlaValLeuGlyAlaGlyLeuTyr 412  
Db 1845 CTGGAGGTGATCCAGATGATGAGGTGGT-----GCCATCTAGGNAAGAGATGTG 1898  
Qy 413 PheGlyGluLeuSerIleLeuAsnLysGlyAsnMetSerGlyAsnArgThrAla 432  
Db 1899 TTTGGGATGTT-----TTCTGGAAGGAGGTACCTCTGACAGCTCGCTGCT 1946  
Qy 433 AsnLysLysSerLeuGlyTyrSerAspLeuPheCysLeuSerLysLysLeuArgGlu 452  
Db 1947 AATGTCCGCGCTTGACCTACTGTGACCTGCGAGTGTCAAGAGGATCCCTGCGAGAA 2006  
Qy 453 ValLeuSerGluTyrProGlnAlaGlnThrIleMetGluGluLysGlyArgGluLeu 472  
Db 2007 GTGCTAGAATCTAC-----ACAGCTTCTCCCTCTCTCCCGGAACCTGATT 2057  
Qy 473 LeuLysMetAsp-----LysLeuAspValAsnAlaGluAlaGluLeuAlaGln 490  
Db 2058 CTCACCTACAATCTGAGGAAGAGGATTTGTTCCGGAAGATCAGCAGCAGTGAACAGAA 2117  
Qy 491 GluAlaThrGluSerArgLeuArg-GlyLeuAspGlnGlnLeuAspAspLeuThrIle 510  
Db 2118 GAA-----GAGGAGGATGAACCGA-----AGAACGAGGCCCCC 2153  
Qy 510 sPheAlaArgLeuLeuAlaGluLeuSerSerAlaLeuLysIleAlaTyrArgIleG 530  
Db 2154 CTTATCTCTCTCTGACCACTGTGACGAGGCTCTTCCAAAGGTTCGCCAGCAGAA 2213  
Qy 530 uArgLeuGluTyrGlnThrArgGlu-TyrProMetPro-GluAspLeuAlaGluAlaAsp 549  
Db 2214 GAAGCCAGGCTGCGACCCGAGAGAGGTGGCGGACCTGGATGACCTG----- 2261  
Qy 550 AspGluGlyGluProGluGlyThrSerLysAspGluGlyArgAlaSer----- 567  
Db 2262 -----GATGTAGAGAGGGAATGCCCTCAGCGACCATACCTCAGCCACACAGC 2312  
Qy 568 -----GlnGluGlyProProGlyPro 574  
Db 2313 CTGGTGAAGCCAGTGTGTGTCACGCTGGTGGTGGAGTCCCGCCAGCCT 2360

RESULT 6  
US-09-694-777A-19  
; Sequence 19, Application US/09694777A  
; Patent No. 6638736  
; GENERAL INFORMATION:  
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
; APPLICANT: STUHRER, WALTER  
; APPLICANT: BECKH, SYNOVE  
; APPLICANT: BRUGEMANN, ANDREA  
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
; APPLICANT: PEREZ, ARACELI SANCHEZ  
; APPLICANT: WESLOH, RUDIGER  
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
; FILE REFERENCE: MPG-8  
; CURRENT APPLICATION NUMBER: US/09/694,777A  
; CURRENT FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 3041  
; TYPE: DNA  
; ORGANISM: Bovine sp.  
US-09-694-777A-19

Alignment Scores:  
Pred. No.: 1,138-37 Length: 3041  
Score: 399.50 Matches: 165  
Percent Similarity: 39.17% Conservative: 119  
Best Local Similarity: 22.76% Mismatches: 263  
Query Match: 13.37% Indels: 180  
DB: 4 Gaps: 30

US-09-927-267-1 (1-575) x US-09-694-777A-19 (1-3041)

Qy 6 LysValLysThrThrGluSerPro----- 14  
Db 559 AAGCGAGAGCTCCACAGCACTCCCTCTGGCGAGGTTCTGCAGCTGGGCTCAGACA 618  
Qy 15 -----ProAlaProSerLysAlaArgLysLeuProValLeuAspProSerGlyAsp 32  
Db 619 TCCTTCCCGAGTACAGCAAGAGGACCAAGACTCCCT-----CGCACATCATCT 669  
Qy 33 TyrTyrTyr-----Tyr-----TyrLeuAsnThrMetValPheProVal 45  
Db 670 TACAC-TACTGGCTTTTAAAGACACGCTGGGACTGGATC-----ATCCTGATCCTAAC 722  
Qy 46 MetTyrAsnLeuIleLeuValCysArgAlaCysPheProAspLeuGlnHisGlyTyr 65  
Db 723 TTTACACAGCCATCTCTGTTCTTACACAGCTCTCTTTAAACACAGGAGCAACAC--- 779  
Qy 66 LeuValAlaTyrLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAspMetVal 85  
Db 780 ---GTGGCTGTGCTGGTGTGGACAGCATCGGGAGTGCATTTTGTGGAGCATTTGG 836  
Qy 86 ValArgPheHisThrGlyPheLeu-----GluGlnGlyIleLeuValValAspLysGlyArg 104  
Db 837 CTGAATTTTACACCATCTTTTGTGGACCCGCTGGGAGGTGATTTCTGACCCCAACATC 896  
Qy 105 IleSerSerArgTyrValArgThrTyrSerPhePheLeuAspLeuAlaSerLeuMetPro 124  
Db 897 ATTGCGATCAACTACTGTAAGACGTGG---TTTGTGATTGACCTTCTGCTCTGTTCGCC 953  
Qy 125 ThrAspValValTyrVal-----ArgLeuGlyProHisThrProThr 138  
Db 954 TATGACGTCAACAGCTTTTGAAGAGTGGATGAGGGGATCATCGACGCTGTTCAGCTCT 1013



Pred. No.: 3.16e-37	Length: 2886
Score: 395.50	Matches: 151
Percent Similarity: 42.30%	Conservative: 118
Best Local Similarity: 23.74%	Mismatches: 266
Query Match: 13.23%	Indels: 102
DB: 4	Gaps: 25

US-09-927-267-1 (1-575) x US-09-694-777A-13 (1-2886)

Qy	11	GlusSerProAlaProSerLysAlaArgLysLeuLeuProValLeuAspProSer	30
Db	575	CAGACATCCCTCCCAGTACAAGCAAGAGCACAAGACTCCCCCTC-----ACA	625
Qy	31	GlyAspTyrTyr-----Tip---TrpLeuSenthThrMetValPhe	43
Db	626	TCATCTTACAT-TATTGTGTTTTTAAGCACCGTGGAATTGGATC-----ATCTTGATC	678
Qy	44	ProValMetTyrAsnLeuIleLeuValCysArgAlaCysPheProAspLeuGlnHis	63
Db	679	TTGACCTTCATACAGCCATCTTGTCCTTATAATGTCCTCTCAAACACGAGCAAT	738
Qy	64	GlyTyrLeuValAlaTrpLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAsp	83
Db	739	AAT-----GTGGCCTGCCTGTTGTGTATAGCATCGTGCATGTTATCTTTTTTGGTGCAC	792
Qy	84	MetValValArgPheHisThrGlyPheLeu---GluGlnGlyLeuLeuValValAspLys	102
Db	793	ATTGTGCTCAATTTTCATACCACCTTGTGTGGACGACGAGGAGGTGATTTCTGACCCC	852
Qy	103	GlyArgIleSerSerArgTyrValArgThrTrpSerPhePheLeuAspLeuAlaSerLeu	122
Db	853	AAACTTATCCGATGAACACTCCTGAACAGCTGG--TTTGATGTGACCTTCTGCTCTGT	909
Qy	123	MetProThrAspValValTyrVal-----ArgLeuGlyProHisThr	136
Db	910	TTGCCATATGATGTCATCAACGCTTTTGAAACGTGGATCAGGCGATCAGACGCTGTTTC	969
Qy	137	ProThrLeuArgLeuAsnArgPheLeuArgAlaProArgLeuPheGluAlaPheAspArg	156
Db	970	AGCTCTCTAAAAGTGTCCGCTCTCCTGTTGGGGGAGTGCCCGCTAAGCTGGACCAC	1029
Qy	157	ThrGluThrArgThrAlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIle	176
Db	1030	TACATTGAATATGGAGCT-----GCTGTGCTGCTCCGCTGGTGTGTGTG 1074	1074
Qy	177	Phe---ValValIleHisTrpAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGly	195
Db	1075	TTTGGGCTGGTGCACACTGATGGCCTGCATCTGTGTACAGCATTTGGGGACTATGAGATC	1134
Qy	196	PheGlyArgasp-----AlaTrpValTyrPro-----Asp	205
Db	1135	TTTGACGAGGACACCAAGACAATCCGCAACACAGCTGGCTGTACCAACTAGCGATGGAC	1194
Qy	206	ProAlaGlnPro-----GlyPheGluArg	213
Db	1195	ATTGGCACCCCTTACCAGTTTAATGGCTTGGCTCAGGGAAGTGGGAAGTGTGCCAGC	1254
Qy	214	LeuArgArgGlnTyrLeuTyrSerPheTyrPheSerThrLeuLeuLeuThrThrValGly	233
Db	1255	AAGAATTTCTGTCTACATCTCCTCGTTTATTTTACAAATGACCAAGCTTCACAGTGGGC	1314
Qy	234	--AspThrProProProAlaArgGluGluTyrLeuPheMetValGlyAspPheLeu	252
Db	1315	TTTGGGAACATCGCCCCATCCAAGACATTGAGAAGATCTTTCAGTGGCCATCATGATG	1374
Qy	253	LeuAlaValMetGlyPheAlaThrIleMetGlySerMetSerSerValIleTyrAsnMet	272
Db	1375	ATTGGCTCACTTCTATATGCCACCATCTTCGGGAATGTGACGACTATTTTCCACAGATG	1434
Qy	273	AsnThrAlaAspAlaAlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeu	292
Db	1435	TATGCCAACACCAACAGATACCATGATGCTCAACAGTGTTCGGGACTTTCTCAAGCTC	1494

## RESULT 8

RESULTS  
US-09-694-777A-1  
; Sequence 1, Application US/09694777A  
; Patent No. 6638736  
; GENERAL INFORMATION:  
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
; APPLICANT: STUHMER, WALTER  
; APPLICANT: BECKH, SYNNOVE  
; APPLICANT: BRUGGEMANN, ANDREA



; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
 ; APPLICANT: PEREZ, ARACELI SANCHEZ  
 ; APPLICANT: WESELOH, RUDIGER  
 ; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: MPG-8  
 ; CURRENT APPLICATION NUMBER: US/09/694,777A  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
 ; PRIOR FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
 ; PRIOR FILING DATE: 1998-04-21  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 3002  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-694-777A-1

Alignment Scores:  
 Pred. No.: 3,38e-37 Length: 3002  
 Score: 395.50 Matches: 151  
 Percent Similarity: 42.30% Conservative: 118  
 Best Local Similarity: 23.74% Mismatches: 266  
 Query Match: 13.23% Indels: 102  
 DB: 4 Gaps: 25

US-09-927-267-1 (1-575) x US-09-694-777A-1 (1-3002)

QY	11	GlusSerProProAlaProSerLysAlaArgLysLeuLeuProValLeuAspProSer	30
DB	611	CAGACATCTCTCCAGGATACAGCAAGGACCAAGACATCCCCCTC-----ACA	661
QY	31	GlyAspTyrTyrTyr-----Trr-----TrrLeuAsnThrMetValPhe	43
DB	662	TCATCTTACAT-TATTGGTGTGTTTAAAGACCAGTGGGATTGGATC-----ATCTTGATC	714
QY	44	ProValMetTyrAsnLeuLeuLeuValCysArgAlaCysPheProAspLeuGlnHis	63
DB	715	TTGACCTTCTATACAGGCATCTTGGTCCCTTATATATGTCCTTCAAAACACGAGCAAT	774
QY	64	GlyTyrLeuValAlaTrrLeuValLeuAspTyrTrrSerAspLeuLeuTyrLeuLeuAsp	83
DB	775	AAT-----GTGGCTCGCTGGTGTGTGATGATCGTGGATGATTAATCTTTTGTGGAC	828
QY	84	MetValValArgPheHisThrGlyPheLeu---GluGlnGlyLeuLeuValValAspLys	102
DB	829	ATTGTGCTCAATTTTTCATACACCTTTGTGGACGAGGAGGAGTGTCTTCTGACCCC	888
QY	103	GlyArgIleSerSerArgTyrTrrValArgThrTrrSerPhePheLeuAspLeuAlaSerLeu	122
DB	889	AAACTATCCGATCACTACTCTGAAGACGTTG---TTTGTGATGACCTTCTGTCTGT	945
QY	123	MetProThrAspValValTyrVal-----ArgLeuGlyProHisThr	136
DB	946	TTGCCATATGATGTCATCAACGCTTTTTCAGAACGTTGATGAGGCAATCAGAGGCTGTC	1005
QY	137	ProThrLeuArgLeuAsnArgPheLeuArgAlaProArgLeuPheGluAlaPheAspArg	156
DB	1006	AGCTCTCTAAAGTTGTCGGCTGCTCGTCTTGGCGAGTGGCCCGTAAGCTGGACCC	1065
QY	157	ThrGluThrArgThrAlaTyrProAsnAlaPheArgIleAlaLysLeuMetLeuTyrIle	176
DB	1066	TACATTGAATATGAGCT-----GCTGTGTGTGTCCTGCTGTGTGTGTG	1110
QY	177	Phe---ValValIleHisTrrAsnSerCysLeuTyrPheAlaLeuSerArgTyrLeuGly	195
DB	1111	TTTGGCTGGCTGCACACTGATGGCTGATCTGGTACACATTTGGGAGTGGGATC	1170
QY	196	PheGlyArgAsp-----AlaTrrValTyrPro-----Asp	205
DB	1171	TTTGACGAGGACCAAGACAATCCGCAACACAGCTGGCTGTGTACCAACTAGCGATGGAC	1230

QY	206	ProAlaGlnPro-----GlyPheGluArg	213
DB	1231	ATTGGCACCCCTTACCACTTTAATGGGTCTGGCTCAGGGAAGTGGGAAGTGGTCCACG	1290
QY	214	LeuArgArgGlnTyrLeuTyrSerPheTyrPheSerThrLeuLeuThrThrValGly	233
DB	1291	AAGAATCTGTCTACATCTCTCTGTTGATTTCATATGACAGCTCACCAGTGTGGGC	1350
QY	234	---AspThrProProAlaArgGluGluTyrLeuPheMetValGlyAspPheLeu	252
DB	1351	TTTGGGAACATCGCCCATCCACAGACATTCGAGAAGATCTTTGAGTGCGCCATCATGATG	1410
QY	253	LeuAlaValMetGlyPheAlaThrIleMetGlySerMetSerSerValIleTyrAsnMet	272
DB	1411	ATTGGCTCACTCTCTATGCGCACCATCTTCGGGAATGTGAGACTATTTCCTCAACAGATG	1470
QY	273	AsnThrAlaAspAlaAlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeu	292
DB	1471	TATGCCAACCAACAGATACCATGAGATGCTCAACAGTGTTCGGACTTCTCGAGCTC	1530
QY	293	GlnHisValAsnArgLysLeuGluArgValIleAspTrrTyrGlnHisLeuGlnIle	312
DB	1531	TACCAGGTGCCAAAGGATTCAGTGACGAGCTAATGGATTATATTGTCTCCACTTGGTCC	1590
QY	313	AsnLysLysMetThrAsnGluValAlaIleLeuGlnHisLeuProGluArgLeuArgAla	332
DB	1591	ATGTCCAGAGGCATTGACACAGAGAAGGTCTCTGCAGATCTGCCCAAGAGATGAGAGCC	1650
QY	333	GluValAlaValSerValHisLeuSerThrLeuSerArgValGlnIlePheGlnAsnCys	352
DB	1651	GACATCTCGTGTCACCTGACCCGCAAGTGTTCAGAGAGCACCCGCGCTTCCGGCTGGCC	1710
QY	353	GluAlaSerLeuLeuGluLeuValLeuLysLeuGlnProGlnThrTyrSerProGly	372
DB	1711	AGTGATGGCTGCTCCGGGCACTGGCCATGGAGTTCACAGCGGTGCTGTCGCCCGG	1770
QY	373	GluTyrValCysArgLysGlyAspIleGlnGluMetTyrIleIleArgGluGlyGln	392
DB	1771	GACCTCATCTACCATGACGAGGAGGAGGCTTGCAGACCTCTGCTTGTGTGTCTGCTCC	1830
QY	393	LeuAlaValValAlaAspAspGlyIleThrGlnTyrAlaValLeuGlyValGlyLeuTyr	412
DB	1831	CTGAGGTGATCCAAAGATGATGAGTGTG-----GCCATCTAGGAAGAAAGGACGCTG	1884
QY	413	PheGlyGluIleSerIleIleAsnIleLysGlyAsnMetSerGlyAsnArgArgThrAla	432
DB	1885	TTTGGAGATGTG-----TTCTGGAAGGAAGCACCCCTTCCAGTCTCTGTGCTC	1932
QY	433	AsnIleLysSerLeuGlyTyrSerAspLeuPheCysLeuSerLysGluAspLeuArgGlu	452
DB	1933	AATGTTAGGCTTGTGACCTACTGTGATCTGTGATCTGATCAAGCGGATGCCCTGCAGAA	1992
QY	453	ValLeuSerGluTyrProGlnAlaGlnThrIleMetGluGluLysGlyArgGluIleLeu	472
DB	1993	GTGCTGGAATCTTAC-----ACGGCTTCTCCCATCTCTCTCCCGAACTGAT	2043
QY	473	LeuLysMetAsn-----LysLeu---AspValAsnAlaGlu	483
DB	2044	CTGACGTACAACTTGAGGAAGAGGATGTGTTCGCGGAAGATCAGCGATGTGAACGTGAA	2103
QY	484	AlaAlaGlu-----	486
DB	2104	GAGGAAGACGCATGAACGAAGAAATGAGGCCCCCTGTATCTTTGCCCGGACCACTC	2163
QY	487	-----IleAlaLeuGlnGluAlaThrGluSerArgLeu-----Arg	498
DB	2164	GTCCGGCCCTCTTCCAGAGATTCGACAGCAGAAAGAGCGCGGCTGGCGAGTGGAGAGA	2223
QY	499	GlyLeuAspGlnGlnLeuAspLeuGlnThrLysPheAlaArgLeuLeuAlaGluLeu	518
DB	2224	GGG---GGCGGAGACCTGGATGATGACCTAGATGTGGAGAGGCAATGTCTTACAGAGCAT	2280

QY 519 GluSerSerAlaLeuLysIleAlaTyrArgIleGluArgLeuGluTyrProGluThrArgGlu 538  
Db 2281 GCCTCCGCCAACCAAGCCTC-----GTGAAGGCCAGCGTGGTCAACGTCGCTGAG 2331  
QY 539 TrpPro---MetProGluAspLeuAlaGluAlaAspAspGluGlyGluProGluGluGly 557  
Db 2332 AGTCCTGCCAGCCCGTATCTTCAGGAGCCTCCACCTCCGGGGTCCAGACCAC--- 2388  
QY 558 ThrSerLysAspGluGluGlyArgAlaSerGlnGluGlyProProGly 573  
Db 2389 ---GCAAGCTACAGGCCAGCGGTCCAGTCCCTGGGCCCCCAAGGG 2433

RESULT 9  
US-09-614-480-1  
; Sequence 1, Application US/09614480  
; Patent No. 6586179  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy James  
; APPLICANT: Liu, Yi  
; APPLICANT: ICigen, Inc.  
; TITLE OF INVENTION: Human Eag2  
; FILE REFERENCE: 018512-00231005  
; CURRENT APPLICATION NUMBER: US/09/614,480  
; CURRENT FILING DATE: 2000-05-29  
; PRIOR APPLICATION NUMBER: US 60/143,467  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2967  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2967)  
; OTHER INFORMATION: human ether a go-go (Eag) 2 voltage-gated  
; OTHER INFORMATION: potassium channel  
US-09-614-480-1

Alignment Scores:  
Pred. No.: 1,78e-36 Length: 2967  
Score: 389.50 Matches: 138  
Percent Similarity: 42.71% Conservative: 108  
Best Local Similarity: 23.96% Mismatches: 250  
Query Match: 13.03% Indels: 80  
Gaps: 20  
DB:

US-09-927-267-1 (1-575) x US-09-614-480-1 (1-2967)

QY 36 TrpTrpLeuAsnThrMetValPheProValMetTyrAsnLeuIleIleLeuValCysArg 55  
Db 655 TGGGTGATTTAATCTTACCTTC-----TACCGCCATATGTTCCCTTATAT 705  
QY 56 AlaCysPheProAspLeuGlnHisGlyTyrLeuValAlaTrpLeuValLeuAspTyrThr 75  
Db 706 GTTCTCTCAACAAAGCAGAACAC-----ATAGCTGCTGCTACTGATAGTGG 759  
QY 76 SerAspLeuLeuTyrLeuLeuAspMetValValArgPheHisThrGlyPheLeuGln 95  
Db 760 GTGGACGTTATTTCTGCTTCATCGTTTAAATTTTCACGACCTTTCGCGGGCCC 819  
QY 96 GlyIleLeuValVal---AspLysGlyArgIleSerSerArgTyrValArgThrTrpSer 114  
Db 820 GTGGAGAGGTATTTCTGACCTTAAGCTCATAGATCACTACTGAAACTTGG---- 876  
QY 115 PhePheLeuAspLeuAlaSerLeuMetProThrAspValValTyrVal----- 130  
Db 877 TTGTGATCGATCTGCTGCTTGTGTTTACCTTATGACATCATCAATGCCCTTTGAAAATG 936  
QY 131 -----ArgLeuGlyProHisThrProThrLeuArgLeuAsnArgPheLeuArgAlaPro 148  
Db 937 GATGAGGAATCAGCAGTCTCTTCAGTCTCTTTAAAGTGGTGGTCTCTTACGATGGGC 996

QY 149 ArgLeuPheGluAlaPheAspArgThrGluThrArgThrAlaTyrProAsnAlaPheArg 168  
Db 997 GTTGGCTAGAAACGACCATTTACCTAGAAATAGGAGCA-----GCA 1041  
QY 169 IleAlaLysLeuMetLeuTyrIlePhe---ValValIleHisTrpAsnSerCysLeuTyr 187  
Db 1042 GTCCCTCGTCTGCTGCTGTGTGTGGTGGTGGCCCACTGGCTGGCTGCATATGG 1101  
QY 188 PheAlaLeuSerArgTyrLeuGlyPheGlyArg-----AspAla 200  
Db 1102 TATGATCATCGAGACTACGAGGTCAATTGATGAAGTCACTAACACCATCAAAATAGACAGT 1161  
QY 201 TrpValTyrPro-----AspProAlaGln----- 208  
Db 1162 TGGCTCTACAGCTGGCTTTGAGCATTTGGGACTCCATATCGCTACATAACAGTCTGGG 1221  
QY 209 -----ProGlyPheGluArgLeuArgArgGlnTyrLeuTyrSerPheTyr 223  
Db 1222 ATATGGGAAGGAGGACCCAGCAAGGATTCATTTG-----TACGTCTCTCTCTCTAC 1272  
QY 224 PheSerThrLeuIleLeuThrThrValGly---AspThrProProAlaArgGluGlu 242  
Db 1273 TTTACCATGACAGCCTTTACCAACCATAGGATTTGGAACATAGCTCTCCACACATGTTG 1332  
QY 243 GluTyrLeuPheMetValGlyAspPheLeuLeuAlaValMetGlyPheAlaThrIleMet 262  
Db 1333 GAGAAGATGTTTTCGTTGGCTATGATGATGTTGGCTCTCTCTTTATGCAACTATTTT 1392  
QY 263 GlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaAlaPheTyrProAsp 282  
Db 1393 GGAATGTTACAAACAATTTTCAGCAATGTATGCCAACACCAACCGCATACCATGAGATG 1452  
QY 283 HisAlaLeuValLysLysTyrMetLysLeuGlnHisValAsnArgLysLeuGluArg 302  
Db 1453 CTGAATAATGTACGGGACTTCTTAAACTATATCAGTCCCAAGGCTTTAGTAGGCGA 1512  
QY 303 ValIleAspTyrTyrGlnHisLeuGlnIleAsnLysLysMetThrAsnGluValAlaIle 322  
Db 1513 GTCATGGATTATTTGTTCTCAACATGGTCCATGTCAAAAGGCATGTATACAGAAAGTGC 1572  
QY 323 LeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSerValHisLeuSerThr 342  
Db 1573 CTCTCCATCTGTCCCAAGACATGAGCTGATATCTGTGTTTCATCTAAACCGGAGGTT 1632  
QY 343 LeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGluGluLeuValLeu 362  
Db 1633 TTTAATGAACATCTCTGCTTTTCGATTGGCCAGGATGGTGTCTCGGCCCTTGGCGGTA 1692  
QY 363 LysLeuGlnProGlnThrTyrSerProGlyGluTyrValCysArgLysGlyAspIleGly 382  
Db 1693 GAGTTCGAACACCATTCATCTGTCTCCCGGGACCTCATTTACCATGCTGGAGAAAGTGG 1752  
QY 383 GlnGluMetTyrIleIleArgGluGlnLeuAlaValAlaAspGlyIleThr 402  
Db 1753 GATGCCCTCTGTTGTGTGTGTCAGGATCTTGGAAAGTCATCCAGGATGATGAGTGGTG 1812  
QY 403 GlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGluIleSerIleIleAsnIleLys 422  
Db 1813 -----GCTATTTAGGAAGGGTGTATGTTTGGAGACATC-----TTCTGG 1854  
QY 423 GlyAsnMetSerGlyAsnArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeu 442  
Db 1855 AAGGAACACCCCTTGGCCATGCATGTGGAACGTCGCGGCACTGACGTACTGTGACCTA 1914  
QY 443 PheCysLeuSerLysGluAspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThr 462  
Db 1915 CACATCATCAAGCGGAAGCCTTGTCTCAAGTCTCTGGACTTTTAT-----ACAGT 1965  
QY 463 IleMetGluGluLysGlyArgGluIleLeuLeuLysMetAsn-----LysLeuAspVal 480  
Db 1966 TTTGCAAACTCTTCTCAGGAATCTCTACTCTTACTTCTGCAATCTGAGGAACGGATCATC 2025  
QY 481 AsnAlaGluAlaAlaGluIleAlaLeuGlnGluAlaThrGluSerArgLeuArgGlyLeu 500

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; SEQ ID NO 6
; LENGTH: 2967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-012-6

Alignment Scores:
Pred. No.: 1,78e-36 Length: 2967
Score: 389.50 Matches: 138
Percent Similarity: 42.71% Conservative: 108
Best Local Similarity: 23.96% Mismatches: 250
Query Match: 13.03% Indels: 80
DB: 4 Gaps: 20

US-09-927-267-1 (1-575) x US-10-162-012-6 (1-2967)
Qy 36 TrpTrpLeuAsnThrMetValPheProValMetTyrAsnLeuLeuLeuLeuValCysArg 55
Db 655 TGGGTGATTTTAAATCTTACCTTC-----TACACCGCCATTATGTTCTTATAAT 705
Qy 56 AlaCysPheProAspLeuLeuHisGlyTyrLeuValAlaTrpLeuValLeuAspTyrThr 75
Db 706 GTTTCCTTCAAAACAAAGCAGCAAC-----ATAGCCTGGCTGTACTCGATAGTGTG 759
Qy 76 SerAspLeuLeuLeuAspMetValValArgPheHisThrGlyPheLeuGluGln 95
Db 760 GTGACGTTATTTTCTGGTTGACATCGTTTAAATTTTACACGACTTTCGTGGGGCCC 819
Qy 96 GlyIleLeuValVal---AspLysGlyArgIleSerSerArgTyrValArgThrTrpSer 114
Db 820 GGTGGAGAGGTCAATTCGTGACCTAAGCTCATAGGATGAACATCTGAAACCTGG--- 876
Qy 115 PhePheLeuAspLeuAlaSerLeuMetProThrAspValValTyrVal----- 130
Db 877 TTTGTGATCGATCGTCTGTTTATCTATGACATCATCAANGCCTTTGAAAGATGTG 936
Qy 131 -----ArgLeuGlyProHisThrProThrLeuArgLeuAsnArgPheLeuAlaPro 148
Db 937 GATGAGGGAATCAGCAGTCTTTCAGTCTTTAAAGTGGTGGCTCTTACGACTGGGC 996
Qy 149 ArgLeuPheGluAlaPheAspArgThrGluThrArgThrAlaTyrProAsnAlaPheArg 168
Db 997 CGTGTGGCTAGGAAACTGGACCATTTACTAGAAATATGAGCA-----GCA 1041
Qy 169 IleAlaLysLeuMetLeuTyrIlePhe---ValIleHisTrpAsnSerCysLeuTyr 187
Db 1042 GTCCTCGTCTCCTGGTGTGTGTTTGGACTGGTGGCCCACTGGCTGGCTGCATATGG 1101
Qy 188 PheAlaLeuSerArgTyrLeuGlyPheGlyArg-----AspAla 200
Db 1102 TATAGCATCGAGACTAGAGGTCAATGATGAAGTCACTAACACCATCCAAATAGACAGT 1161
Qy 201 TrpValTyrPro-----AspProAlaGln----- 208
Db 1162 TGGCTCTACAGCTGGCTTTTGGACATGGGACTCCATATCGCTACAATACCAAGTGGG 1221
Qy 209 -----ProGlyPheGluArgLeuArgGlnTyrLeuTyrSerPheTyr 223
Db 1222 ATATGGGAAGGAGGAGCCAGCAAGGATTCATTG-----TACGTGTCTCTCTCTAC 1272
Qy 224 PheSerThrLeuIleLeuThrValGly---AspThrProProAlaArgGluGlu 242
Db 1273 TTTACCATGACAGCCCTTACACCATAGGATTTGGAACACATAGCTCTTACCAGATGTG 1332
Qy 243 GluTyrLeuPheMetValGlyAspPheLeuLeuAlaValMetGlyPheAlaThrIleMet 262
Db 1333 GAGAAGATGTTTCGGTGGCTATGATGATGTTGGCTCTCTCTTCTTATGCAACTATTTT 1392
Qy 263 GlySerMetSerSerValIleTyrAsnMetAsnThrAlaAspAlaPheTyrProAsp 282
Db 1393 GGAATGTTACACAAATTTTCCAGAAATGTTATGCCAACCAACCATGATGATGATG 1452
Qy 283 HisAlaLeuValLysLysTyrMetLysLeuGlnHisValAsnArgLysLeuGluArgArg 302
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## RESULT 10

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US-10-162-012-6
; Sequence 6, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
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Db 1453 CTGAATATGACGGAGCTCTCTAAACTCTATCATGCTCCAAAGGCTTAGTGAGCGA 1512
Qy 303 ValIleAspTyrGlnHisLeuGlnIleAsnLysMetThrAsnGluValAlaIle 322
Db 1513 GTCATGGATTATTTGTCTCAACATGCTCCATGTCAAAGGCAATGATACAGAAAGGTC 1572
Qy 323 LeuGlnHisLeuProGluArgLeuArgAlaGluValAlaValSerValHisLeuSerThr 342
Db 1573 CTCTCCATCTGTCCCAAGAGATGAGAGCTGATATCTGTGTCTCAATCAACCGGAGGTT 1632
Qy 343 LeuSerArgValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGluGluLeuValLeu 362
Db 1633 TTTAATGAACATCTCTTCGATGTCGCCAGCATGGGTCTCTCGCGCTTGGCGGTA 1692
Qy 363 LysLeuGlnProGlnThrTyrSerProGluGluTyrValCysArgLysGlyAspIleGly 382
Db 1693 GAGTTCACCAACCATTCACATGCTCTCCGGGACCTCATTTACCATGCTGGAGAAAGTGTG 1752
Qy 383 GlnGluMetTyrIleIleArgGluGluGlnLeuAlaValValAlaAspAspGlyIleThr 402
Db 1753 GATGCCCTCTCTGTGTGTGATGCTCTTGGAGTCATCCAGGATGATGAGTGTGTG 1812
Qy 403 GlnTyrAlaValLeuGlyAlaGlyLeuTyrPheGlyGluIleSerIleIleAsnIleLys 422
Db 1813 -----GCTATTTAGGAAGGTCATCTATTGGAGATC-----TTCTGG 1854
Qy 423 GlyAsnMetSerGlyAsnArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeu 442
Db 1855 AAGAAACACCCCTTCCCATGTCATGTCGCAACCTCCGGGACCTGACGACTGTGACCTA 1914
Qy 443 PheCysLeuSerLysGluAspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThr 462
Db 1915 CACATCATCAAGCGGAGAGCTTGTCTCAAGTCCTGGACTTTAT-----ACAGCT 1965
Qy 463 IleMetGluGluLysGlyArgGluIleLeuLeuLysMetAsn-----LysLeuAspVal 480
Db 1966 TTTCGAAACTCTCTCTCAAGAACTCTCACTCTTCTGCAATCTGAGGAACGGATCATC 2025
Qy 481 AsnAlaGluAlaAlaGluIleAlaLeuGlnGluAlaThrGluSerArgLeuArgGlyLeu 500
Db 2026 TTTCGTAAGATCATGATGTGTAAGAAAGAGAG-----GAGGAGCGCTCCGG----- 2073
Qy 501 AspGlnGlnLeuAspAspLeuGlnThrLysPheAlaArgLeuLeuAlaGluLeuGluSer 520
Db 2074 -----CAGAGAAATGAGGTGACCTCAGCATTCCTCGTGAGCCAC 2112
Qy 521 SerAlaLeuLysIleAlaTyrArgIleGluArgLeuGluTyrGlnThrArgGluTyrPro 540
Db 2113 CCAGTCAGAAAGCTCTTCCAGAGTTCAAGCAG-----2145
Qy 541 MetProGluAspLeuAlaGluAlaAspAspGluGlyGluProGluGluGlyThrSerLys 560
Db 2146 CAGAGGAGCTCGGAATCAAGGCTCAACAGGCTGACCTCGCTGAGAGG---AACCACATC 2202
Qy 561 AspGluGluGlyArgAlaSerGlnGluGly-ProProGlyProGlu 575
Db 2203 CAGGTAGAGACCGCTCTCTACAGATGAGAACCTCCATCCACCGGAA 2248
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## RESULT 11

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US-10-162-012-4
; Sequence 4, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
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Alignment Scores:

Pred. No.:	2,43e-36	Length:	3553
Score:	389.50	Matches:	138
Percent Similarity:	42.71%	Conservative:	108
Best Local Similarity:	23.96%	Mismatches:	250
Query Match:	13.03%	Indels:	80
DB:	4	Gaps:	20

US-09-927-267-1 (1-575) x US-10-162-012-4 (1-3553)

Qy 36 TrpTrpLeuAsnThrMetValPheProValMetTyrAsnLeuIleLeuValCysArg 55  
932 TGGGTGATTTTAAATCTTACCTTC-----TACACCGCATATGTTCTTATAAT 982	
Qy 56 AlaCysPheProAspLeuGlnHisGlyTyrLeuValAlaTrpLeuValLeuAspTyrThr 75	
983 GTTTCCTTCAAAACAAAGCAGACAAC-----ATAGCCTGGCTGCTGATGTGTG 1036	
Qy 76 SerAspLeuLeuTyrLeuLeuAspMetValValArgPheHisThrGlyPheLeuGluGln 95	
Db 1037 GTGACGCTTATTTCTGTTGATCGTTTAAATTTTCAACGACTTTCGTGGGGCCC 1096	
Qy 96 GlyIleLeuValVal---AspLysGlyArgIleSerArgTyrValArgThrTrpSer 114	



Db 626 TCATCTTACAT-TATGTGTTTAAAGACCGTGGATTGGATC-----ATCTTGATC 678  
QY 44 ProValMetTyrAsnLeuLeuValCysArgAlaCysPheProAspLeuGlnHis 63  
Db 679 TTGACCTTCTATACACCATCTTGGTCCCTTATATATGCTCTCTCAAAACAGGAGAT 738  
QY 64 GlyTyrLeuValAlaTrpLeuValLeuAspTyrThrSerAspLeuLeuTyrLeuAsp 83  
Db 739 AAT-----GTGGCTCGCTGCTGTTGATAGCATCGTGGATGTTATCTTTTGTGGAC 792  
QY 84 MetValValArgPheHisThrGlyPheLeu---GluGlnGlyIleLeuValValAspLys 102  
Db 793 ATTGTGCTCAATTTTCATACCACTTTGTGGACCAAGGAGGAGTGTCTGACCCC 852  
QY 103 GlyArgIleSerSerArgTyrValArgThrTrpSerPhePheLeuAspLeuSerLeu 122  
Db 853 AAACCTTATCCGATCACTACCTGAAGACGTGG---TTTGTGATTGACCTTCTGTCTGT 909  
QY 123 MetProThrAspValVal----- 128  
Db 910 TTGCCATATGATGATCATCAACGCTTTTGAGAACGTGGATGAGTTAGTGCCTTTATGGGT 969  
QY 129 -----TyrValArgLeuGlyProHisThrPro----- 137  
Db 970 GATCCAGGGAAGATTGGTTTCTGTCATCAGATTCCACCACCTCGGAGGAGAGAGAT 1029  
QY 138 -----ThrLeuArgLeuAsnArgPheLeuArgAlaProArg 149  
Db 1030 CAGGCAATCAGCAGCCTGTTTCTGCTCTCTAAAGTTGTCCGCTCTCTCGCTTGGGCGA 1089  
QY 150 LeuPheGluAlaPheAspArgThrGluThrArgThrAlaTyrProAsnAlaPheArgIle 169  
Db 1090 GTGGCCCTAGCTGAGCACCTACATTGAATATGGAGCT-----GCTGTG 1134  
QY 170 AlalysLeuMetLeuTyrIlePhe---ValValIleHisTrpAsnSerCysLeuThrPhe 188  
Db 1135 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194  
QY 189 AlalysSerArgTyrLeuGlyPheGlyArgAsp-----AlaTrp 201  
Db 1195 AGCATTTGGGACTATGAGATCTTTTACGAGGACACCAAGACAATCCGCAACACAGCTGG 1254  
QY 202 ValTyrPro-----AspProAlaGlnPro----- 209  
Db 1255 CTGTACCAATAGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1314  
QY 210 -----GlyPheGluArgLeuArgGlnTyrLeuTyrSerPheTyrPheSerThr 226  
Db 1315 AAGTGGGAAGGTGGTCCAGCAAGAAATCTGTCTACATCTCTCTGTTGTTTACCAATG 1374  
QY 227 LeuIleLeuThrValGly---AspThrProProAlaArgGluGluGluTyrLeu 245  
Db 1375 ACCAGCTTCACAGCTGGTGGCTTTGGGAACATCGCCCATCCACAGACATTGAGAAGATC 1434  
QY 246 PheMetValGlyAspPheLeuAlaValMetGlyPheAlaThrIleMetGlySerMet 265  
Db 1435 TTTGAGTGGCCATCATGATGATGGTCACTTCTATGACCACTTCTGGGAATGTG 1494  
QY 266 SerSerValIleTyrAsnMetAsnThrAlaAspAlaPheTyrProAspHisAlaLeu 285  
Db 1495 ACGACTATTTTCAACAGATGATGCCAACCAACACAGATACCATGAGATGCTCAACAGT 1554  
QY 286 ValLysLysTyrMetLysLeuGlnHisValAsnArgLysLeuGluArgValIleAsp 305  
Db 1555 GTTCGGGACTTCTGGAAGCTTACAGGTGCCAAAGAGGATGAGTGACGAGATGATGAT 1614  
QY 306 TrpTyrGlnHisLeuGlnIleAsnLysLysMetThrAsnGluValAlaIleLeuGlnHis 325  
Db 1615 TATATTGTCTCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1674  
QY 326 LeuProGluArgLeuArgAlaGluValAlaValSerValHisLeuSerThrLeuSerArg 345

Db 1675 TGCCCCAAGGACATGAGACCCGACATCTGCGTGCACCTGACCCGCAAGGTGTTCAAGGAG 1734  
QY 346 ValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGluLeuValLeuLysLeuGln 365  
Db 1735 CACCGCGCTTCCGCGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1794  
QY 366 ProGlnThrTyrSerProGlyGluTyrValCysArgLysGlyAspIleGlyGlnGluMet 385  
Db 1795 ACGTGTCACTGTGCCCCAGGGGACCTCATCTACCATGACGAGAGAGCGTTGACACGCTC 1854  
QY 386 TyrIleLeuArgGluGlyGlnLeuAlaValAlaAspAspGlyIleThrGlnTyrAla 405  
Db 1855 TGCITTTGTGGTTTCTGGCTCCCTGGAGGTGATCCAAGATGATGAGTGGTG-----GCC 1908  
QY 406 ValLeuGlyAlaGlyLeuTyrPheGlyGluLeuSerIleLeuAsnIleGlyGlyAsnMet 425  
Db 1909 ATTCTAGAAAGAGAGACGTGTTTGGAGATGTG-----TTCTGGAAGGAAGGCC 1956  
QY 426 SerGlyAsnArgArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeuPheCysLeu 445  
Db 1957 ACCTTGCCCCAGTCTGTGCCAATGTAGGCGCTTACCTACTGTGATCTGATGTGATGTATC 2016  
QY 446 SerLysGluAspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThrIleMetGlu 465  
Db 2017 AAGCGGATGCCCTGCAGAAAGTGTGGAATTCTAC-----ACGCGCTTCTCCCAT 2067  
QY 466 GluLysGlyArgGluLeuLeuLysMetAsn-----Lys 477  
Db 2068 TCCTTCTCCCGAACCTGATCTGACGTACAACTTGAGGAAGAGATGTTGTTCGGAAG 2127  
QY 478 Leu---AspValAsnAlaGluAlaGlu----- 486  
Db 2128 ATCAGCATGTGAACGTGAAGAGAACGATGAAACGAAGAATGAGGCCCCCTG 2187  
QY 487 -----IleAlaLeuGlnAlaThrGlu 494  
Db 2188 ATCTTGCCCCGACCCCTGTCCGCGCTCTTCCAGAGATTCGACAGACAGAAAGAG 2247  
QY 495 SerArgLeu-----ArgGlyLeuAspGlnLeuAspLeuGlnThrLysPhe 511  
Db 2248 GCCAGCTGGCAGCTGAGAGAGG---GGCCGCGACCTGGATGACCTAGATGTGGGAAG 2304  
QY 512 AlaArgLeuLeuAlaGluLeuGluSerAlaLeuLysIleAlaTyrArgIleGluArg 531  
Db 2305 GGCAATGTCTTACAGACATGCTCCGCCAACACAGCCCTC-----GTGAAGGCC 2355  
QY 532 LeuGluTrpGlnThrArgGluTrpPro---MetProGluAspLeuAlaGluAlaAspAsp 550  
Db 2356 AGCTGTGTACCGTGGTGGAGAGTCTTCCACGCGCTATCTTCCAGGACGCTCCACC 2415  
QY 551 GluGlyGluProGluGluGlyThrSerLysAspGluGluGlyArgAlaSerGlnGluGly 570  
Db 2416 TCCGGGTGCCAGCACAC-----GCAAGATGACAGCGCGCGAGTCCGAGTCCGTGGGC 2469  
QY 571 ProProGly 573  
Db 2470 CCCAAGGG 2478

## RESULT 13

US-09-694-777A-2

; Sequence 2, Application US/09694777A

; Patent No. 6638736

; GENERAL INFORMATION:

; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL

; APPLICANT: STUHMER, WALTER

; APPLICANT: BECKH, SYNNOVE

; APPLICANT: BRUGGEMANN, ANDREA

; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO

; APPLICANT: PEREZ, ARACELI SANCHEZ

; APPLICANT: WESELOH, RUDIGER

; TITLE OF INVENTION: NOVEL HUMAN K<sup>+</sup> ION CHANNEL AND THERAPEUTIC APPLICATIONS

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: MFG-8

1291	Db	CTGTACCAACTAGCGATGGACATTTGGCACCCCTTACCCAGTTTAAATGGGTCTGGCTCAGGG	1350
210	Qy	-----GlyPheGluArgLeuArgGlnTyrLeuTyrSerPheTyrPheSerThr	226
1351	Db	AAATGGGAAGGTGGTCCACGCAAGAAATTCGTGCTACATCTCCCTCGTGTGTTATTTCACAATG	1410
227	Qy	LeuIleuThrThrValGly-----AspThrProProAlaArgGluGluTyrLeu	245
1411	Db	ACCAGCCTCACCAGTGTGGGCTTTGGGAACATCGCCCATCCACACAGCATTTGAGAAGATC	1470
246	Qy	PheMetValGlyAspPheLeuLeuAlaValMetGlyPheAlaThrIleMetGlySerMet	265
1471	Db	TTTGCAATGCCATCATGATGATGTGGCTCACTTCTATGCCACCATCTTCGGGAATGTG	1530
266	Qy	SerSerValIleTyrAsnMetAsnThrAlaAspAlaPheTyrProAspHisAlaLeu	285
1531	Db	ACCATATTTTCCACAGATGTATGCCAACACCAACAGATACCATCAGATGCTCAACAGT	1590
286	Qy	ValIysIleTyrMetLysLeuGlnHisValAsnArgLysLeuGluArgValIleAsp	305
1591	Db	GTTCGGGACTTCTGAAGCTTCTACCAAGTCTCACCAGGTGCCAAAAGGATTTGATGTAGCGAGTAATCGAT	1650
306	Qy	TrpTyrGlnHisLeuGlnIleAsnLysLysMetThrAsnGluValAlaIleLeuGlnHis	325
1651	Db	TATATTGTGTCCACTTGGTCCATGTCCAGAGGCAATTGACACAGAGAAGTCTCGCAGATC	1710
326	Qy	LeuProGluArgLeuArgAlaGluValAlaValSerValHisLeuSerThrLeuSerArg	345
1711	Db	TGCCCCAAGACATAGAGCCGACATCTCGCTGCACCTGAACCGCAAGGTGTTCACAGAG	1770
346	Qy	ValGlnIlePheGlnAsnCysGluAlaSerLeuLeuGluLeuValLeuLysLeuGln	365
1771	Db	CACCGGCTTCGGGCTGGCCAGTATGGCTCGGGCACTGGCCATGGAGTTCACG	1830
366	Qy	ProGlnThrTyrSerProGlyGluTyrValCysArgLysGlyAspIleGlyGlnGluMet	385
1831	Db	ACGGTGCACTGTGCCCCAGGGGACCTCATCTACCATGCAGAGAGAGCGTTGACAGCCTC	1890
386	Qy	TyrIleIleArgGluGlyGlnLeuAlaValValAlaAspGlyIleThrGlnTyrAla	405
1891	Db	TGCTTTGTGTTCTTGCTCCCTCGGAGGTGATCCAAAGATCATGAGTGGTG-----GCC	1944
406	Qy	ValLeuGlyAlaGlyLeuTyrPheGlyGluIleSerIleIleAsnIleLysGlyAsnMet	425
1945	Db	ATTCTAGGAAAAGAGACGCTTTTGAGATGTG-----TTCTGGAAGGAAGCC	1992
426	Qy	SerGlyAsnArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeuPheCysLeu	445
1993	Db	ACCTTGTCCCAAGTCCTGTGCAATGTTAGGCGCTTGACCTACTGTCTATCTGTCATGTATC	2052
446	Qy	SerLysIleAspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThrIleMetGlu	465
2053	Db	AACGGGATGCCCTGCAGAAAGTCTGGAAATCTTAC-----ACGGCCTTCTCCCAT	2103
466	Qy	GluLysGlyArgGluIleLeuLeuLysMetAsn-----Lys	477
2104	Db	TCCTTCTCCGGAACCTGATCTTGACGTACAATCTGAGGAAGAGGATTGTGTTCGGAAG	2163
478	Qy	Leu---AspValAsnAlaGluAlaGlu-----	486
2164	Db	ATCAGCGATGTGAACGCTGAAGAGGAAGAACGCATGAACCGAAAGAATGAGGCCCCCTG	2223
487	Qy	-----IleAlaLeuGlnGluAlaThrGlu	494
2224	Db	ATCTTCCCCCGGACCAACCTGTCTCGGCGCTCTTCCAGAGATTCGCACAGAGAAGAG	2283
495	Qy	SerArgLeu-----ArgGlyLeuAspGlnLeuAspLeuThrLysPhe	511
2284	Db	GCCAGGCTGGCAGTGGAGAGGG-----GGCCGGGACTTGGATGACCTAGATGTGGGAAG	2340
512	Qy	AlaArgLeuLeuAlaGluLeuGluSerSerAlaLeuLysIleAlaTyrArgIleGluArg	531

Db 2341 GGCAATGCTTTACAGAGCATGCTCCGCCAACACACAGCCTC-----GTGAAGGCC 2391  
Qy 532 LeuGluTrpGlnThrArgGluTrpPro---MetProGluAspLeuAlaGluAlaAsp 550  
Db 2392 AGCGTGGTCAACGTCGTGAGAGTCTCCACGCCGCTATCCTTCCAGGCAGCCTCCACC 2451  
Qy 551 GluGlyGluProGluGluGlyThrSerLysAspGluGluGlyArgAlaSerGlnGluGly 570  
Db 2452 TCCGGGTGCCAGACCAC-----GCAAGCTACAGGCCCGCAGGTCGAGTCCGCTGGGC 2505  
Qy 571 ProProGly 573  
Db 2506 CCCAAGGG 2514

## RESULT 14

US-09-600-776-9

; Sequence 9, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 3715  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-600-776-9

## Alignment Scores:

Pred. No.:	1,876-35	Length:	3715
Score:	382.50	Matches:	143
Percent Similarity:	40.06%	Conservative:	107
Best Local Similarity:	22.92%	Mismatches:	221
Query Match:	12.80%	Indels:	153
DB:	4	Gaps:	22

US-09-927-267-1 (1-575) x US-09-600-776-9 (1-3715)

Qy 71 ValLeuAspTyrThrSerAspLeuLeuTyrLeuLeuAspMetValValArgPheHisThr 90  
Db 942 GTCTGTGACCTGGCGTGAAGTCTCTTCATCTTAGATATTGTGCTGAATTTTCGTACT 1001  
Qy 91 GlyPheLeu---GluGlnGlyLeuValValAspLysGlyArgLysSerArgTyr 109  
Db 1002 ACATTTGTCAAGTCAGGTCAGGTGTATTGCGCCCAAGTCCATTGGCTCCACTAC 1061  
Qy 110 ValArgThrTrpSerPhePheLeuAspLeuAlaSerLeuMetProThrAspValValTyr 129  
Db 1062 GTCACCACTGG---TTCTGTGATGTATAGCAGCACTGCCCTTTTGGACTACTACAT 1118  
Qy 130 -----ValArgLeuGlyProHisThrProThrLeuArgLeuAsnArgPhe 144  
Db 1119 GCCTTCAAGGTCAATGTGTAGCTTGGGGCTCAC-----CTACTGAAGACCGTGGGGCTG 1172  
Qy 145 LeuArgAlaProArgLeuPheGluAlaPheAspArgThrGluThrArgThrAlaTyrPro 164  
Db 1173 CTTCGGCTGTCCGCTACTACCAAGACTGACCGGTACTCTCAGTAGGCTGTT--- 1229  
Qy 165 AsnAlaPheArgIleAlaLysLeuMetLeuTyrIlePheValValIle---HisTrpAsn 183  
Db 1230 -----GTGCTCACCTTGCTCATGGTGTGTTGGCTGCTGCCCACTGGGTG 1277  
Qy 184 SerCysLeuTyrPheAlaLeuSerArgTyrLeuGly-----TACATCGGCCAGCAAGATTGAGAACAGCGAG 1325  
Db 1278 GCCTGCGTTTGGTTC-----TACATCGGCCAGCAAGATTGAGAACAGCGAG 1325

Qy 196 -----PheGlyArgAspAlaTrpValTyr----- 203  
Db 1326 TCAGAGTGCCTGAGATCGGCTGGCTGCAGAGCTGGCAGGAGCTGGAGAGCGCCTAT 1385  
Qy 204 -----ProAspProAlaGlnPro----- 209  
Db 1386 TACCTGGTGAGCCGGAGTCCAGATCGAGGGAACAGCTCTGGCCAGAGTGAACACTGCAGT 1445  
Qy 210 -----GlyPheGluArg 213  
Db 1446 AGCAGTGGCGGCGCAGCAACCGGACTGGGCTGGAGCTCTGGTGGCCCATCC 1505  
Qy 214 LeuArgArgGlnTyrLeuTyrSerPheTyrPheSerThrLeuIleLeuThrValGly 233  
Db 1506 CTACGAGCGCTACATCACTCTTGTACTTTCGCTCAGAGTCTCACCAGTGTGGC 1565  
Qy 234 AspThrProProAlaAarg---GluGluGluTyrLeuPheMetValGlyAspPheLeu 252  
Db 1566 TTCGGCAATGTTCGCTTAACACAGACACTGAGAAGATTTCCTCATCTGCACCATGCTT 1625  
Qy 253 LeuAlaValMetGlyPheAlaThrIleMetGlySerMetSerSerValIleTyrAsnMet 272  
Db 1626 ATTGGAGCTCTGATGCATCGATGCTGTTGGGAATGTGACAGCCATCATCCAGCGCATG 1685  
Qy 273 AsnThrAlaAspAlaAlaPheTyrProAspHisAlaLeuValLysLysTyrMetLysLeu 292  
Db 1686 TAGCTCGCCCTTCTGTACACAGCGCACCCTGACCTGGAGACTACATTCGCATC 1745  
Qy 293 GlnHisValAsnArgLysLeuGluArgValIleAspTyrTyrGlnHisLeuGlnIle 312  
Db 1746 CACCGCATCCCAAGCCCTCAAGCAGCGCATGTCGAGTACTTCCAAAGCCACCTGGGCC 1805  
Qy 313 AsnLysLysMetThrAsnGluValAlaIleLeuGlnHisLeuProGluArgLeuAla 332  
Db 1806 GTGAACACAGCGCATGCATCACCAGCTGTGTCGAGAGCTTCCGGATGAGTTGAGCA 1865  
Qy 333 GluValAlaValSerValHisLeuSerThrLysSerArgValGlnIlePheGlnAsnCys 352  
Db 1866 GACATCGCCATGACCTGCACAGAGGTCCTG---CAGCTGCCATTTTCGAGCAGCG 1922  
Qy 353 GluAlaSerLeuLeuGluValLysLysLeuGlnProGlnThrTyrSerProGly 372  
Db 1923 AGCCGTGGCTCGCTGGGGCACTGTCTCTGCCCTGAGCGCCGCTTCTGCACGCGCGGC 1982  
Qy 373 GluTyrValCysArgLysGlyAspIleGlyGlnGluMetTyrIleIleArgGluGlyGln 392  
Db 1983 GAGTACCTCATTCACCAAGCGGATGCTCTCAGGCTCTCTACTTTGTGTCTCAGTTCC 2042  
Qy 393 LeuAlaValAlaAlaAspAspGlyIleThrGlnTyrAlaValLeuGlyValGlyLeuTyr 412  
Db 2043 ATGGAGGTCTTC-----AAGGTGGCACCTCTCGCCATTTAGGGAAGGGTCACTG 2096  
Qy 413 PheGly-----GluIleSerIleIleAsnIleLysGlyAsnMet 425  
Db 2097 ATCGGCTGTGAGTGCCTCCAGCAGAGCAAGTA-----GTGAAGGCCAAT--- 2141  
Qy 426 SerGlyAsnArgArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeuPheCysLeu 445  
Db 2142 -----GCCGACGTAAAGGGGTGACATACTCGCTCTCAGTCCGCTG 2183  
Qy 446 SerLysGluAspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThrIleMetGlu 465  
Db 2184 CAGTGGCTGGCTGCGCAGAGCGCTGCACCTGTACCTGTAGTTTGGCCAGCTTTAGC 2243  
Qy 466 GluLysGlyArgGluIleLeuLeuLysMetAsnLysLeuAspValAsnAlaGluAla 485  
Db 2244 CGTGGCTCCGA-----GGGAGGCTCAGCTACAACTGGAGCTGGA 2285  
Qy 486 GluIleAlaLeuGlnGluAlaThrLysSerArgLeuArgGlyLeuAspGlnLeuAsp 505  
Db 2286 GGAGTGTCTGCAGAGTGGATACAGCTCA---CTGAGTGTGTGACACACCTCATGTCC 2342





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QY 415 -----GluIleSerIleIleAsnIleLysGlyAsnMetSerGlyAsn 428
Db 1942 GAGCTGCCCGGGGAGCAGGTG-----GTAAAGGCCAAT----- 1977
QY 429 ArgArgThrAlaAsnIleLysSerLeuGlyTyrSerAspLeuPheCysLeuSerLysGlu 448
Db 1978 -----GCCGAGTGAAGGGGTGACGTACTCGTCTCGCTGCAGTGTCTGCAGCTGGCT 2028
QY 449 AspLeuArgGluValLeuSerGluTyrProGlnAlaGlnThrIleMetGluGluLysGly 468
Db 2029 GGCCTGCACGACAGCAGCTTGGCTGTACCGCGAGTTTGGCCCGCGCTTC---AGTCGTGGC 2085
QY 469 ArgGluIleLeuLeuLysMetAsnLysLeuAspValAsnAlaGluAlaGluIleAla 488
Db 2086 CTCGAGGGGAGCTCAGTCAAC---CTGGGTGTGGGGAGGCTCTGCAGAGGTG--- 2139
QY 489 LeuGlnGluAlaThrGluSerArgLeuArgGlyLeuAspGlnGlnLeuAspLeuGln 508
Db 2140 -----GACACCAGCTCCCTGAGCGCGACAATACCCCTTATGTCCACGCTGGAG 2187
QY 509 ThrLys----- 510
Db 2188 GAGAAGGAGACAGATGGGAGCAGGGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCC 2247
QY 511 -----PheAlaargLeuLeuAla 516
Db 2248 TCCAGCCCCCTGCTGCCCTGGTGGTGACCTCCTCATCTAGCTGCCAAGCTGTATCC 2307
QY 517 GluLeuGluSerSer----- 521
Db 2308 CCACGTGGAACAGCACCCCGGCTCGTCTAGTGTGCAGAGGGAGGCCAGGGCAGGG 2367
QY 522 AlaLeuLysIle-----AlaTyrArgIleGluArgLeuGluTrp 534
Db 2368 GCTTTGAAGGCTGAGGCTGGCCCTCTGCTCCCCACGGGCCCTAGAGGGGCTACGGCTG 2427
QY 535 GlnThrArgGluTyrProMetProGluAspLeuAlaGluAlaAspAspGluGlyGluPro 554
Db 2428 CCCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGGGTAGTAGTGGC---ATT 2484
QY 555 GluGluGlyThrSerLysAspGlu-----GluGlyArgAlaSerGlnGluGlyPro 571
Db 2485 GAAGACGGCTGTGGCTCGACCAAGCCCAAGTTCTCTTCCGGCTGGGCCAGTCTGGCCCG 2544
QY 572 -----ProGlyProGlu 575
Db 2545 GAATGTAGCAGCAGCCCCCTCCCTGGACACAG 2577
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Job time : 202 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 18:43:39 ; Search time 164.122 Seconds  
(without alignments)  
7804.118 Million cell updates/sec

Title: US-09-927-267-2

Perfect score: 2308

Sequence: 1 agagggaggaggaacag.....agactgcatccatctaa 2308

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*

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5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	78.4	3.4	1307	4	US-09-172-422-3
2	70.2	3.0	1507	4	US-08-997-685A-5
3	65.8	2.9	1790	4	US-08-997-685A-11
4	59.8	2.6	3480	3	US-09-226-012-1
5	59.8	2.6	3950	3	US-09-226-012-3
6	56	2.4	1584	4	US-08-997-685A-3
7	53.6	2.3	3249	4	US-09-358-383C-3
8	53.6	2.3	3355	4	US-09-358-383C-1
9	52.8	2.3	7218	1	US-08-232-463-14
10	52.4	2.3	7218	1	US-08-232-463-14
11	52	2.3	3249	4	US-09-343-494-2
12	52	2.3	3323	4	US-09-600-776-1
13	50.8	2.2	3041	4	US-09-694-777A-19
14	50.4	2.2	3857	4	US-09-336-643A-19
15	49.8	2.2	3064	4	US-09-600-776-5
16	49	2.1	3141	2	US-08-956-242-1
17	49	2.1	3141	3	US-09-351-215-1
18	45.2	2.0	8495	4	US-09-797-906-3
19	45	1.9	505	4	US-09-621-976-15639
20	44	1.9	4722	4	US-08-979-608A-14
21	44	1.9	4722	4	US-09-517-849-14
22	44	1.9	4722	4	US-09-616-289-14
23	42.8	1.9	818	3	US-08-205-697A-4
24	42.8	1.9	818	3	US-08-702-525-4
25	42.8	1.9	818	4	US-08-837-867A-4
26	42.8	1.9	818	5	PCT-US95-02576-4
27	42.8	1.9	1570	3	US-08-205-697A-10

28	42.8	1.9	1570	3	US-08-702-525-10	Sequence 10, Appl
29	42.8	1.9	1570	4	US-09-837-867A-10	Sequence 10, Appl
30	42.8	1.9	1570	5	PCT-US95-02576-10	Sequence 10, Appl
31	42.8	1.9	1606	3	US-08-702-525-64	Sequence 64, Appl
32	42.8	1.9	1606	5	PCT-US95-02576-64	Sequence 64, Appl
33	42.8	1.9	1888	3	US-08-205-697A-1	Sequence 1, Appl
34	42.8	1.9	1888	3	US-08-702-525-1	Sequence 1, Appl
35	42.8	1.9	1888	4	US-09-837-867A-1	Sequence 1, Appl
36	42.8	1.9	1888	5	PCT-US95-02576-1	Sequence 1, Appl
37	42.8	1.9	2516	3	US-08-205-697A-3	Sequence 3, Appl
38	42.8	1.9	2516	3	US-08-702-525-3	Sequence 3, Appl
39	42.8	1.9	2516	4	US-09-837-867A-3	Sequence 3, Appl
40	42.8	1.9	2516	5	PCT-US95-02576-3	Sequence 3, Appl
41	42.8	1.9	2886	4	US-09-694-777A-13	Sequence 13, Appl
42	42.8	1.9	2967	4	US-09-694-777A-14	Sequence 14, Appl
43	42.8	1.9	3002	4	US-09-694-777A-1	Sequence 1, Appl
44	42.8	1.9	3083	4	US-09-694-777A-2	Sequence 2, Appl
45	41.8	1.8	364	4	US-09-621-976-17202	Sequence 17202, A

## ALIGNMENTS

### RESULT 1

US-09-172-422-3

; Sequence 3, Application US/09172422A

; Patent No. 6300485

; GENERAL INFORMATION:

; APPLICANT: Adams, Arwen E.

; APPLICANT: Chiu, Choi Ying

; APPLICANT: Duhl, David

; APPLICANT: Gorman, Susan W.

; APPLICANT: Leng, Song

; APPLICANT: Sheffield, Val

; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED

; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF

; FILE REFERENCE: 200130.442

; CURRENT APPLICATION NUMBER: US/09/172.422A

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 1307

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(1307)

; OTHER INFORMATION: n = A,T,C or G

US-09-172-422-3

Query Match 3.4%; Score 78.4; DB 4; Length 1307;

Best Local Similarity 46.6%; Pred. No. 1.6e-11;

Matches 324; Conservative 0; Mismatches 366; Indels 6; Gaps 2;

QY 832 TTCGATTCGCAAGCTGATGCTTTACATTTTGTGTCATCCATTCATGGAACAGTGCCTAT 891

Db 590 TGCATCATGTAACCTCATCGCATGATGCTCTCTGCTCTGCCACTGGGACGGCTGCCTGC 649

QY 892 ACTTTGCCCTATCCCGTACTCGGCTTGGCGGTGACGATGGTGTACCCGACCCCG 951

Db 650 AGTTCTGGTACCCATCTACAGACTTCCTGTGACTGCTGGGTGTCCATCAACAAC 709

QY 952 CGAGCCTGGCTTTGAGCGCTGCGGCGCAGTAGTACCTCTATAGCTTTTACTTCTCCAGC 1011

Db 710 TGGTGAACAACCTCTCTGGG---GAAGCAGTACTCTTAGCGCTCTTCAAGCCATGACC 766

QY 1012 TGATACCTGACTACGTGGGGGATACACCGCGCGCAGCCAGGAAGAGATCCTCTTCA 1071

Db 767 ACATGCTGTGATCGGCTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 826

Qy	1072	TGTTGGCGGACTTCCTCTGCTGGCGGTATGGGTTTCGCCACCATCATCGGTAGCATGAGCT	1131
Db	827	CCATGCTCAGCATGATCGTGGGTGCCACCTGCTACGCCATGTTTCATTTGGCCACGCCACTG	886
Qy	1132	CTGTCACTTCAACATCAACACTGCAGATCGGCTTTCTACCCAGATCATGCACTGGTGA	1191
Db	887	CCCTCATTCAGTCCTGGATCTCTCCGGGCGCCAGTACAGGAAAGTACAACACAGGTGG	946
Qy	1192	AGAAGTACATGAAGCTCGACACGTCACACGTCGAAGCTGGAGCGCGAGTTATTGACTGGT	1251
Db	947	AGCAGTACATGTCCTTTTCAAGCTCCGCGCCGACACCCGCGCAGCGCATCCACGACTACT	1006
Qy	1252	ATCAGCACCTTCAGATCAAACAAGAGATGACCAACGAGGTAGCCATCTTACACACTTGC	1311
Db	1007	ACGAGCACCGCTA---CCAGGGCAAGATGTTCCAGCAGGAGAGACCCCTGGGCGAGCTAA	1063
Qy	1312	CTGAGCGGCTGCGGGCAGAAGTGGCTGTGCTGTGCACCTGTCCACTCTGAGCGCGGTGC	1371
Db	1064	GCAGCCCTGCGGGAGGAGATCATCAACTTTAACTGTGCGAAGCTGGTGGCCCTCCATGC	1123
Qy	1372	AGATCTTTCAAGACTGTGAGGCCAGCCTGCTGGAGGAGCTGTGTCTGAAGCTGCAGCCCC	1431
Db	1124	CACGTGTTGCCAATTCGGGACCCCAACTTCGTGAGTCCATGCTGACCAAGCTCGTTCG	1183
Qy	1432	AGACCTACTCACAGGTGAATATGTATGCCCGCAAAAGGAGACATTGGCCAAAGAGATGTACA	1491
Db	1184	AGGTCTTCCAGCTGGGGACTCATCATCCTCGGGAAGGCACATTGGCAAGAATGTACT	1243
Qy	1492	TCATTCGAGAGGGTCAACTGGCGGTGGTCAGATG	1527
Db	1244	TCATTCAGCATGGCGGTGAGGTGAGGTGCTCAGGTGCTCACCAGG	1279

## RESULT 2

US-08-997-685A-5  
; Sequence 5, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandel, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1507  
; TYPE: DNA  
; ORGANISM: mouse;  
US-08-997-685A-5

Query Match	3.0%	Score 70.2;	DB 4;	Length 1507;
Best Local Similarity	46.1%	Pred. No. 2.9e-09;		
Matches 351;	Conservative	0;	Mismatches 398;	
			Indels 12;	Gaps 3;

[illegible]

Qy 892 ACTTTGCCCTATCCCGGTACCTGGGCTTCGGGGGTGACGCATGGGTGTACCCGACCCCG 951

Db 763 AGTTCCTAGTCCCATGCTGCTGAGAGACITCCCCCATGACTGCTGGGTGTCCATCATGGCA 822

Qy 952 CGAGCCTGGCTTTAGAGGCCCTGGGGCCGACGTAACCTCTATAGCTTTACTTCTCACGC 1011

Db 823 TGGTGAATACTCTCTGGGGNAGAGTATCTCTACGCCCTCTTCAAGGCCATGAGCCACA 882

Qy	1012	TGATACTGACTACAGTGGGCGATACACGGCGCCAGCCAGGAGAGAGATCACTCTTCA	1071
Db	883	TGCTGTGCATTGGGTATGCGCGGCGAGCACCCGTAGGCATGCTGACGCTGGGTCA	942
Qy	1072	TGCTGGGCGCAATTCTGTGTGCGCGCTATGGGTTTTGGCCACCACATCGGTAGCATGAGCT	1131

		943	TGCTCAGCATGATCGTGGGGGC---CACCTGCTATGCCATGTTCATGGCCACGCCACTG	939
Qy		1132	CTGTCACTACAACGAACACTGCAGATCGCGCTTTACCACAGATCATGCACCTGGTGA	1191
Db		1000	CCCTCATCCAGTCGCTAGACTCTCCCGGGCCAGTACCAAGAGAAGTATAAACAGGTGG	1059
Qy		11192	AGAAGTACATGAAGCTGCAGACGTCACACGCAAGCTGGAGCGCGAGTTATTGACTGGT	1251
Db		1060	AGCAGTACATGTCCTTTCCACAAGCTCCGCGCTGACACCCGACAGCGCATCCATGACTACT	1119
Qy		1252	ATCAGCACCTGCAGATCAACAAGAAGATGACCAACAGAGTAGGCATCTTACAGCACTTGC	1311
Db		1120	ATGAACACCCGTTA---CCAAGGCAAGATGTTTGATGAGGAAGCATCCTGGGTGAGTTGA	1176
Qy		1312	CTGAGCGCTCGCGGACAGAAGTCGTGTCTGTGCACCTGTCCACTCTCAGCGCGGTGC	1371
Db		1177	GTGAGCCACTTCGAGAGGAGATCATCAACTTTAACTGCCGAAGCTGGTGGCATCATGC	1236
Qy		1372	AGATCTTTCAAGAACTGTGAGGCCAGCGCTGCTGAGGAGCTGTGCTGAACTCGACGCC	1431
Db		1237	CACCTGTTTGCCAAACGCGAGATCCCAAACCTTTGTGACATCCATGCTGACCAAGTTGCGTTTCG	1296
Qy		1432	AGACCTACTCACAGGTGATATGTATCGCGAAGAGAGACATGGCCAGAGATGTACA	1491
Db		1297	AGGTCTTTCAGCCTCGGGGATTATCATATCCGCGAAGGCACCATTCGGCAAGAATGTACT	1356
Qy		1492	TCATCCGAGAGGCTCAACTGGCCGTGTGGCAGATGATGGTATCACACAGTATGCTGTGC	1551
Db		1357	TTATCCAGCAGCGGTGGTCAAGCTGCTACTAAGGG-----CAACAAAGACACAGGC	1410
Qy		1552	TCGGTCAGGGCTCTACTTTTGGGAGATCAGCATCATCAAC	1592
b		1411	TGGCTGATGCTCTATATTTGGAGAGATCTGCTTGCTGACC	1451

### RESULT 3

US-08-937-685A-11  
; Sequence 11, Application US/08997685A  
; Patent No. 6551821  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University  
; APPLICANT: Kandell, Eric  
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof  
; FILE REFERENCE: 0575/54806  
; CURRENT APPLICATION NUMBER: US/08/997,685A  
; CURRENT FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1790  
; TYPE: DNA  
; ORGANISM: human;  
US-08-937-685A-11

Query Match	2.9%	Score 65.8;	DB 4;	Length 1790;
Best Local Similarity	45.4%	Pred. No. 5.1e-08;		
Matches 361;	Conservative	0;	Mismatches 42;	Indels 12;
				Gaps 3;

**Qy** 835 GCATTGCCAAGCTGATGCTTTTACATTTTTCTCGTCATCOATGGAAACAGCTGCCTATACT 894  
|||||  
**Db** 660 GGATCTGCATCTCATCAGCATGATGTGCTGTCTGCCACTGGGACGGCTGCTTGCACT 719

Qy 895 TTGCCCTATCCCGGTACCTGGGCTTGGGCGTCAACGATGGGTGATCCCGACCCCGCGC 954

Db 720 TCTGGTGCCATGCTCTCAGACCTTCCCGCGCACTCTGGGTGTCATCAATGGGATGG 779

Qy 955 AGCTGCTTTGAGCGCCTCGCGGCCAGTACCTCTATAGCTTTTACTTCTCCACGCTGA 1014  
Db 780 TGAACCACTCGTGAGTGAACGTG---TACTCTTCGCACCTCTTCAGGCCCATAGCCACA 836  
Qy 1015 TACTGACTACAGTGGCGGATACACCGCGCCAGCGGAAGAAGTAGTACCTCTTCATGG 1074

837 TGCTGTGCATCGGTAGTGGCGGCGAGCGCCGGAAGCATGACGGACATCTGGCTGACCA 896  
1075 TGGCGACTTCTCTGCTGGCGGTGATGGTTTGGCCACATCATGGGTAGATGAGCTGTG 1134  
897 TGCTCAGCATGATGTGGGTGCCACTGCTACGCCATGTTTCATCGGCCAGCCCACTGCC 956  
1135 TCATCTACAACATGAACATGACATGCGGTCTTCTACCCAGATCATGCACTGGTGAAGA 1194  
957 TCATCTCAGTCTGCTGATCTCTCGGGCGCCGATACAGGAGATCAAGCAGGTGGAGC 1016  
1195 AGTACATGAAGCTGACGACATCAACCGCAAGCTGGAGCGCGAGTATTGACTGGTATC 1254  
1017 AGTACATGCTCTTCCACAGCTGCCAGTGAATCTCCGCCAGAAATCCACGACTACTATG 1076  
1255 AGCACTTGCAGATCAACAGAGATGACCAAGAGTACCAAGAGTACCACTTACAGCACTTGGCTG 1314  
1077 AACACCGTTA---CCAGGGCAAGATGTTTGACGAGGACAGCATCTCGGGGAGCTCAACG 1133  
1315 AGCGGCTGCGGGGAGAGTGGCTGTGTGTGACCTGTCTGACCTGTGAGCGGGTGCAGA 1374  
1134 GGCCCTTGGGGAGAGATGCTCAACTTCACTGCCGAGAGCTGGTGGCTTCCATGGCG 1193  
1375 TCTTTCAAGACTGTAGGCCAGCTGCTGGAGGAGTGGTGTGAACTGCAGCCCGAGA 1434  
1194 TGTTCGCCAAGCGCGACCCCAACTTCTGTCAGCGCATGTGACCAAGCTCAAGTTTCGAGG 1253  
1435 CTTACTCACCAGTGAATATGTATGCCGCAAGAGACANTGGCCAGAGATGTACATCA 1494  
1254 TCTTCCAGCGGGTGAATACATCATCCGCGAAGCACCANTCGGGAAGAGATGACTTCA 1313  
1495 TCCGAGAGGGTCAACTGCGCGTGTGGCAGATGATGTATCACACATGTCTGTGTCTG 1554  
1314 TCCAGCAGCGGTGTGAGCTGCTCACTAAGG-----CAACAAAGAGATGAGTGT 1367  
1555 GTGCGAGGCTCTACTTTGGGAGATCAGCATCATCAACATCAAGGGAACATGTCTGGGA 1614  
1368 CCGATGCTCTCTACTTCCGGGAGATCTGCCTGTCTCACCGGGGCGCGCGACGCGAGCT 1427  
1615 ACCGCCGACAGCCA 1629  
1428 GCGGGCTGACACCTA 1442

RESULT 4  
US-09-226-012-1  
; Sequence 1, Application US/09226012  
; Patent No. 6207383  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/226,012  
; CURRENT FILING DATE: 1999-01-06  
; EARLIER APPLICATION NUMBER: 09/122,847  
; EARLIER FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3480  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3477)  
US-09-226-012-1

Query Match  
Best Local Similarity 45.9%; Pred. No. 3e-06;  
Matches 205; Conservative 0; Mismatches 242; Indels 0; Gaps 0;  
1058 AGAGTACTCTTTCATGTGGGCGAGTCTCTGCTGCGCGTCACTGGTTCGCCACCATCAT 1117

1908 AGAAGATCTTCTCCATCTGGCTCATCTGCTTGGCTCCCTCATGTATGTAGCACTT 1967  
1118 GGTAGCATGAGCTCTGTCTATCTAACAATGAACATGCGAGATGCGGCTTTCTACCCAGA 1177  
1968 CGGCAAGCTGTGGCCATCATCCAGCGGTGTACTCGGGGACAGCCCGCTACCAACACA 2027  
1178 TCATGCACTGGTGAAGATGACATGAAGCTGCGACAGTCAACCGCAAGCTGGAGCGGCG 1237  
2028 GATGCTCGGGTGGGAGTTCATCCGCTTCCACAGATCCCCAATCCCCCTGGCCAGCG 2087  
1238 AGTTATTGACTGGTATCAGCACTGCGAGATCAACAAGAAGATGACCAACAGAGTAGCCAT 1297  
2088 CTTGAGGAGTACTTCCAGCAGCGCTGCTCTACACCAACGGCATCGCATGAACGGGT 2147  
1298 CTTACAGCATTTGCTGAGCGGTGCGGGCAGAGTGGTGTGTGTGCACTGTCCAC 1357  
2148 GCTGAAGGGCTTCCCTGAGTGCCTGCAAGGTGACATCTGCTGCACTGAACCGCTCACT 2207  
1358 TCTGAGCGGGTGCAGATCTTTCAGAACTGTGAGGCCAGCTGCTGGAGGAGCTGTGCT 1417  
2208 GCTGAGCATGTCAAAACCTTCCGAGGGGCCAACAGGGTGTGCTTGGGGCCCTTGGCCAT 2267  
1418 GAAGCTGACGCGCCAGACCTACTTACCAGGTGAATATGTATGCCGCAAGAGAGACATTGG 1477  
2268 GAAGTTCAAGACACACATGACACCGCCAGGGGACACACTGGTGCATGCTGGGACCTGCT 2327  
1478 CCAAGAGATGTACATCATCCGAGAGG 1504  
2328 CACGCGCTGTACTTCTATCTCCCGGG 2354

RESULT 5  
US-09-226-012-3  
; Sequence 3, Application US/09226012  
; Patent No. 6207383  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/226,012  
; CURRENT FILING DATE: 1999-01-06  
; EARLIER APPLICATION NUMBER: 09/122,847  
; EARLIER FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 3950  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(3543)  
US-09-226-012-3

Query Match  
Best Local Similarity 45.9%; Pred. No. 3.2e-06;  
Matches 205; Conservative 0; Mismatches 242; Indels 0; Gaps 0;  
1058 AGAGTACTCTTTCATGTGGGCGAGTCTCTGCTGCGCGTCACTGGTTCGCCACCATCAT 1117  
1974 AGAAGATCTTCTCCATCTGCGTCACTGCTGCTCCCTCATGTATGTAGCATCTT 2033  
1118 GGTAGCATGAGCTCTGTCTATCTAACAATGAACATGACAGTGCAGATGCGGCTTTTACCCAGA 1177  
2034 CGGCAAGCTGTGGCCATCATCCAGCGGTGTACTCGGGCAGACCGCCGCTTACCAACACA 2093  
1178 TCATGCACTGGTGAAGAGTACATGAAGTGCAGCAGCTCAACCGCAAGCTGGAGCGGCG 1237  
2094 GATGCTCGGGTGGGAGTTCATCCGCTTCCACAGATCCCCAATCCCCCTGGCCAGCG 2153

Qy	1238	AGTTATTGAC	TGGTATCAG	CACTGAC	ATCAACAAG	ATGACAA	CGAGGTAG	CCCAT	1297
Db	2154	CCTCGAGGAG	TACTTCCAG	CACGCGCT	TGCTCTAC	CAACGCG	CATCGAC	ATGAACGCGGT	2213
Qy	1298	CTTACAGCAC	TTCGCTGAG	CGGCTCG	CGGCGAG	AAGTGGT	GTGTCTGT	GTCACCTG	1357
Db	2214	GCTGAAGGG	CTTCCCTG	AGTGCCT	GAGGTGAC	ATCTGCCT	GACCTGA	ACCGTCACT	2273
Qy	1358	TCTGAGCGG	TGTCAGAT	CTTTTCA	GAACGTG	TGAGCC	AGCCTGT	GCGAGGAG	1417
Db	2274	GCTCGACAC	TGCAAA	CCCTTCC	GAGGGCC	CAACAA	GGCGTC	GCCTTGGG	2333
Qy	1418	GAAGCTG	CAGCCCC	CAGACCT	ACTACTCA	CAGGTGA	TATGTAT	CCGCAAGG	1477
Db	2334	GAAGTTCA	AGACCA	CACATG	CACCGCC	AGGGACA	CTGGTG	CACTGTGGG	2393
Qy	1478	CCAAGAG	ATGTAC	ATCATCC	GAGAGG				1504
Db	2394	CACGCGC	CTGTACT	TTCATCT	CCCCGGG				2420

## RESULT 6

RESULT 6  
US-08-997-685A-3  
; Sequence 3, Application US/08997685A

FACE NO. 0331821  
: GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University

APPLICANT: Kandel, Eric

APPLICANT: KANDEL, ERIC  
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof

; TITLE OF INVENTION: BRAIN  
: FILE REFERENCE: 0575/54806

FILE REFERENCE: 05/5/54806  
CURRENT APPLICATION NUMBER: IIS/00/007 608A

; CURRENT APPLICATION NUMBER: US/0  
: CURRENT FILING DATE. 1992.12.12

; CURRENT FILING DATE: 199  
 ; NUMBER OF SEC ID NOS: 60

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: E  
: GEO ID NO 3

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; SEQ ID NO 3
: 1 ENCTH 1584

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; LENGTH: 15  
: TYPE: DMS

; TYPE: DNA

; ORGANISM: mou

Query Match 2.4%; Score 56; DB 4; Length 1584;  
Best Local Similarity 44.5%;  
Pred. No. 2.3e-05;  
Matches 310; Conservative 0; Mismatches 380; Indels 6;  
Gaps 2;

832	Qy	TTGCGATTGCCAAGCTGATGCTTTACAAATTTTGTGCGTCATCCATTGGAACAGCTGCGCTAT	891
566	Db	TGGCGACTCTGTAACTTGAATCAGATGATGCTACTGTCTGCCATCGGACGGTTCCTGCTG	625
892	Qy	ACTTTTGGCCCTATCCCGGTACTCTGGCTTCGGGGCTGACGCTATGGGTGTACCCGGACCCCG	951
626	Db	AGTTCCTGGTGGCCATGCTCAAGACTTCCCCAGCGACTCTGGGTGTCCATCAACAACA	685
952	Qy	CGCAGCTGTGCTTTGAGCGCTCGGGCGCCAGTACTCTATAGCTTTTACTTCTTCCACGCG	1011
686	Db	TGTTGAACCACTCGTGGAGC--GAGCTCTACTCGTTCGGCTCTTCAAGGCCATGAGCC	742
1012	Qy	TGATATGACTACAGTGGGGCGATACACCGCGCCGACGCCGGAAGAGATGACTTTTCA	1071
743	Db	ACATGCTGTGCATCGGCTACGGCGCGCAGCGCCCGAGAGCATGACAGATCTGGGTGA	802
1072	Qy	TGTTGGCGGACTTCTGCTCGCGCTGATGGTTTCGCCACCATCATGGGTAGCATGAGCT	1131
803	Db	CCATGCTCAGCATGATCGTAGGGCCCACTGCTATGCCATGTTCTTTGGGCAAGCCACTG	862
1132	Qy	CTGTCACTTCAACATGAACACTGCAGATCGGCTTTCTACCCAGATCATGCACTGGTGA	1191
863	Db	CGGCTCATCCAGTCCCTGGATTGCTGACGGCGCCCAATACCAGGAGAAAGTCAAGCAAGTAG	922
1192	Qy	AGAAGTATCATGAAGCTGCAGCAGCTCAACCGCAAGCTGGAGCGCGAGTTATTGACTGGT	1251
923	Db	AGCAATACATGTCTCTTCCAAACACTGCCCGCTGACTTCGCCGCAAGAGATCCACGATTACT	982
1252	Qy	ATCAGCACCTTGCAGATCAACAAGAAGATGACCAACGAGGTAGGCATCTTACAGCACTTGC	1311

## RESULT 7

RESULT /  
US-09-358-383C-3  
; Sequence 3, Application US/09358383C

FACE NO. 05183398  
GENERAL INFORMATION:

: APPLICANT: Curtis. Royv A. J

APPLICANT: CULLIS, ROY A.J.  
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; TITLE OF INVENTION: NOVEL  
: FILE REFERENCE: MNT-055CD

FILE REFERENCE: MNI-055CP  
CURRENT APPLICATION NUMBER: IIS/00/059 3020

; CURRENT APPLICATION NUMBER: US/0  
: CURRENT FILING DATE: 1999-07-21

; CURRENT FILING DATE: 1999-07-21  
 ; PRIORITY APPLICATION NUMBER: USCN 08/118 855

; PRIOR APPLICATION NUMBER: USS  
PRIOR FILING DATE: 1998-07-31

; PRIOR FILING DATE: 1998-07-  
 NUMBER OF CEO ID NO. 20

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Pat

; SEQ ID NO 3

; LENGTH: 3249

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; TYPE: DNA

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; ORGANISM: *Macaca* sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1

Query Match	2.3%	Score 53.6;	DB 4;	Length 3249;
Best Local Similarity	45.6%;			
Pred. No. 0.00015;				
Matches 268;	Conservative	0;	Mismatches 314;	Indels 6;
				Gaps 2;

Qy	943	CGAACCCGCGAGCCTGGCTTTGAGCGGCTGCGCGCCAGTACCTCTATAGCTTTTACT	1002
Db	1313	CGGGGTGGAGCTGCTAGGCGGCCCTCGCTGCGCAGCGCTACATCACCTCCCTCTACT	1372
Qy	1003	TCCTCCAGCTGATACTGACTACAGTGG--CGATACACGCCGCCAGCCAGGGAAGAAG	1059
Db	1373	TCGCACTCAGCAGCCTCACACGGCTGGGCTTGGCAAGTGTCGGCAACACGGCACTG	1432
Qy	1060	AGTACCTCTTTCATGTTGGCGCACTTCCTGTGTCGCCGTATGGTTTTCGCCACCATCATGG	1119
Db	1433	AGAAGATCTTCTCCATCTGCACCATCTCATCGCGCCCTGATGCACGCGTGGTGTTCG	1492
Qy	1120	GTAGCATGACTCTGTCTATCTACAAATGAACACTGCAGATGGCGCTTTCTACCCAGATC	1179
Db	1493	GGAACTGACGGGCATCATCCAGCGGATGTAGCGCGCGCTTTCTGTACCAACAGCGCA	1552
Qy	1180	ATGCATCTGTGTGAAGAAGTACATGAAGCTCAGCACGTCAAACGCAAGCTGGAGCGCGAG	1239
Db	1553	CGCGGACCTGCGCGACTACATCCGATCCACGGTATCCCAAGGCCCTCAAGCAGCGCA	1612
Qy	1240	TTATTGACTGGTATCAGCACCTGCAGATCAAACAGAAATGACCAACGAGGTAGCCATCT	1299
Db	1613	TGCTGGAGTACTTCCAGGGCCACTGGGGGGTGAACAATGGCATTCGACAACAACGAGCTGC	1672
Qy	1300	TACAGCACTTGCCTGAGCGGCTCGCGGCAGAAAGTGCTGTGTGTGCACCTGTCCACTC	1359







Db 1493 GGAACGTGAAGCCATCATCCAGCGCATGTAGCCCGCGCTTCTGTACACAGCCGCA 1552  
Qy 1180 ATGCACCTGGTGAAGAAGTACATGAGCTGACGAGCTGACCGCAAGTGTGAGCGGCGAG 1239  
Db 1553 CGCGGACCTTCCGCGACTACATCCGATCCACCGGTATCCCAAGCCCTCAAGCAGCGCA 1612  
Qy 1240 TTATTGACTGTATCAGCACCTGCAGATCAACAAGAGATGACCAAGAGGTAGCCATCT 1299  
Db 1613 TGCTGGAGTACTTCCAGCCACCTGGCGGCTGGAATGAGATCGACACCGAGGTGC 1672  
Qy 1300 TACAGCACTTGCCTGAGCGGCTGGCGGAGAGTGGCTGTCTGTGCACTGTCCACTC 1359  
Db 1673 TGCAGAGCTTCCCTGACGAGCTGGCGGAGACATCGCCATGCATCGACAAGGAGTCC 1732  
Qy 1360 TGACCCGGTGCAGATCTTTCAGAACTGTGAGGCGAGCCTCTGAGAGAGTGTGTCTGA 1419  
Db 1733 TG---CAGCTGCOACTGTTTGAAGCGGCCAGCCGCGGTGCTGCGGCACTGTCTCTGG 1789  
Qy 1420 AGCTGCAGCCCGACACTTACACAGGTGATATGTATGTCGCGCAAGGAGACATTTGCC 1479  
Db 1790 CCTTGGCGCGCGCTTCTGACGCGCGGCGAGTACCTCATCCACAGGCGATGCCCTGC 1849  
Qy 1480 AAGAGATGTATCATCATCGAGAGGTCAACTGGCGGTGGTGGCAGATG 1527  
Db 1850 AGGCCCTCTACTTTGTCTGCTCTGCTCCATGGAGGTGCTCAAGGGTG 1897

## RESULT 12

US-09-600-776-1

; Sequence 1, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PC  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3323  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)..(3257)  
US-09-600-776-1

Query Match 2.3%; Score 52; DB 4; Length 3323;  
Best Local Similarity 45.4%; Pred. No. 0.00041;  
Matches 267; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

Qy 943 CGGACCCGCGCAGCCTGGCTTTGAGCGCTGGCGCGCAGTACTCTATAGCTTTTACT 1002  
Db 1318 CGGGCTGGAGCTGCTGGCGCGCCGCTGCTGTCGAGCGCTACATCACCTCCCTCTACT 1377  
Qy 1003 TCTCCACGCTGATCTACTACAGTGGG---CGATACACCGCGCGCAGCGGGAAGAG 1059  
Db 1378 TCGCACTCAGAGCCTCACCAGCGTGGCTTGGCAACAGTGTCCGCAACACGACACCG 1437  
Qy 1060 AGTACCTTTTCATGGTGGCGACTTCTGTGGCGCTCATGGGTTTGGCCACCATCATGG 1119  
Db 1438 AGAAGATCTTCTCCATCTGCACCATGTCTATCGCGCGCTGATCCACGCGGTGTGTG 1497  
Qy 1120 GTAGCATGAGCTCTGTCTATCTACAACTGAACACTGACAGATGCGGCTTTCTACCCAGATC 1179  
Db 1498 GGAACGTGACGCCATCATCCAGCGCATGTACGCGCGCGCTTCTGTGTACACAGCGCGCA 1557

Qy 1180 ATGCACCTGGTGAAGAAGTACATGAGCTGACGAGCTGACCAAGCGAGCTGGAGCGCGAG 1239  
Db 1558 CGCGGACCTTCCGCGACTACATCCGATCCACCGGTATCCCAAGCCCTCAAGCAGCGCA 1617  
Qy 1240 TTATTGACTGTATCAGCACCTGCAGATCAACAAGAGATGACCAAGAGGTAGCCATCT 1299  
Db 1618 TGCTGGAGTACTTCCAGGCCACCTGGCGGCTGGAATGAGATCGACACCGAGGTGC 1677  
Qy 1300 TACAGCACTTGCCTGAGCGGCTGGCGGAGAGTGGCTGTCTGTGCACTGTCCACTC 1359  
Db 1678 TGCAGAGCTTCCCTGACGAGCTGGCGGAGACATCGCCATGCATCGACAAGGAGTCC 1737  
Qy 1360 TGACCCGGTGCAGATCTTTCAGAACTGTGAGGCGAGCCTCTGAGAGAGTGTGTCTGA 1419  
Db 1738 TG---CAGCTGCOACTGTTTGAAGCGGCCAGCCGCGGTGCTGCGGCACTGTCTCTGG 1794  
Qy 1420 AGCTGCAGCCCGACACTTACACAGGTGATATGTATGTCGCGCAAGGAGACATTTGCC 1479  
Db 1795 CCTTGGCGCGCGCTTCTGACGCGCGGCGAGTACCTCATCCACAGGCGATGCCCTGC 1854  
Qy 1480 AAGAGATGTATCATCATCGAGAGGTCAACTGGCGGTGGTGGCAGATG 1527  
Db 1855 AGGCCCTCTACTTTGTCTGCTCTGCTCCATGGAGGTGCTCAAGGGTG 1902

## RESULT 13

US-09-694-777A-19

; Sequence 19, Application US/09694777A  
; Patent No. 6638736  
; GENERAL INFORMATION:  
; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL  
; APPLICANT: STUHRER, WALTER  
; APPLICANT: BECKH, SYNNOVE  
; APPLICANT: BRUGEMANN, ANDREA  
; APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO  
; APPLICANT: PEREZ, ARACELI SANCHEZ  
; APPLICANT: WESELOH, RUDIGER  
; TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: MFG-8  
; CURRENT APPLICATION NUMBER: US/09/694,777A  
; CURRENT FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: PCT/EP99/02695  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EP 98 10 7268.9  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 3041  
; TYPE: DNA  
; ORGANISM: Bovine sp.  
US-09-694-777A-19

Query Match 2.2%; Score 50.8; DB 4; Length 3041;  
Best Local Similarity 44.5%; Pred. No. 0.00083;  
Matches 245; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

Qy 984 TACCTCTATAGCTTTTACTTCTCCACGCTGATCTACTACTAGTGGGCG---GATACACCG 1040  
Db 1305 TACATCTCTCTGTTGTTATTTTCCATGACCGCTCACCAGCGTGGGCTTTGGAAACATC 1364  
Qy 1041 CGCGCAGCAGGGAAGAGTACCTTTCATGGTGGCGACTTCTCTGTGGCGGTGATG 1100  
Db 1365 GCCTCGTCCACAGACATTTGAGAAGATCTTTGCGGTGGCCATCATGATGTTGGCTCCCTC 1424  
Qy 1101 GGTTCGCCACCATCATGGGTAGCATGAGCTGTCTATCTTACACATGACACTGACATG 1160  
Db 1425 CTCTATGCCACCATCTTTGGGAATGTGACGACCATTTTCCAAACAGATGTACGCCAACACC 1484  
Qy 1161 GCGGCTTTTACCCAGATCATGCACCTGGTGAAGAAGTACATGAAGCTGACGAGCTCAAC 1220  
Db 1485 AACAGGTACCATGAGATGCTCAACAGTGTCCGGGACTTCTTTGAAGCTTCTACAGGTGCC 1544

QY 1221 CGAAGCTGAGCGCGAGTTATTGACTGGTATCAGACCTGCAGATCAACAAGAGATG 1280  
Db 1545 AAGGGCTGACGAGCGAGTATGATGATACATCGTGTCCATGTCAGAGGC 1604  
QY 1281 ACCAAGAGGTAGCCATCTTACAGACATGCTGAGCGGCTGCGGCGAGAAGTGGCTGTG 1340  
Db 1605 ATTGACACAGAGAGGTCTGAGATCTGCCCAAGGACATGAGAGCGGATCTGCGTG 1664  
QY 1341 TCTGTGACCTGTGCACTCTGAGCGGCTGAGATCTTTTCAAGACTGTGAGCGCCAGCTG 1400  
Db 1665 CACCTAAACCGAAGGTCTTCAAGAGACACCGAGCTTTTCCGCTGGCCAGCGAGCTG 1724  
QY 1401 CTGAGGAGCTGCTGCTGAAGCTGAGCGCCAGACCTACTCAGAGTGAATATCTATGC 1460  
Db 1725 CTGCGGACCTGGCCATGAGTTCAGACCGTGTGCACTCGGCCCTGGGAGCTCATCTAC 1784  
QY 1461 CGCAAGAGAGACATTTGGCACAAGAGATGTACATCATCCGAGAGGTCACCTGGCGCTGTG 1520  
Db 1785 CACGAGGGAGAGCGTGCAGACGCTGTGCTTCGTGTCTCCGGCTCCCTGGAGTGATC 1844  
QY 1521 GCAGATGATG 1530  
Db 1845 CAGGATGACG 1854

## RESULT 14

US-09-336-643A-19  
; Sequence 19, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 3857  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (249)...(3495)  
; OTHER INFORMATION: K+Hnov14  
US-09-336-643A-19

Query Match 2.2%; Score 50.4; DB 4; Length 3857;

Best Local Similarity 45.2%; Pred. No. 0.0012;

Matches 266; Conservative 0; Mismatches 316; Indels 6; Gaps 2;

QY 943 CGGACCCCGCAGCTCGCTTTGAGCGCTTGGCGCGCAGTACCTCTATAGCTTTTACT 1002  
Db 1558 CGGGCTGAGTGTGCGGCGCCGTGCTGCGAGCGCTTACATACCTCCCTCTACT 1617  
QY 1003 TCTCACGCTGATCTACTACAGTGGG---CGATACCGCGCCGACCGCAGGGAAG 1059  
Db 1618 TCGCACTCAGCAGCTCACCAGCTGGGCTTCGGCAACGCTGTCGCCAACACGGACACG 1677  
QY 1060 AGTACCTCTTATGTGGCGACTCTCTGCTGCGCGCTCATGGTTTCGCCACCATG 1119  
Db 1678 AGAAGATCTTCTCCATCTGSCACCATGCTCATCGCGCGCTGATGACGCGGTGGTGTG 1737

QY 1120 GTAGCATGAGCTGTCTCATCTACACATGAACATGCAGATGCGGCTTTCTACCCAGATC 1179  
Db 1738 GGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGGCTTTCTGTACACAGCCGCA 1797  
QY 1180 ATGCACTGGTGAAGAAGTACATGAAGCTGCAGCACGTCAACCCGAAAGCTGGAGCGCGAG 1239  
Db 1798 CGCGGACCGCGGCACTACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCA 1857  
QY 1240 TTATGTAGTGTATCAGCACTGCAGATCAACAAGAGATCAACCAAGAGTAGGCATCT 1299  
Db 1858 TGCTGGAGTACTTCCAGGCCACTTGGCGGTGGAACAATGGCATCGACACCAAGAGTGC 1917  
QY 1300 TACAGCACTTCCCTGAGCGGCTGCGGCGAGAGTGGTGTCTGTGCACCTGTCCACTC 1359  
Db 1918 TGCAGAGCTCCCTGACGAGCTGCGCGAGACATGCCCATGACCTGCACAAAGAGGTCC 1977  
QY 1360 TGAGCGGGTGCAGATCTTTTCAAGAACTGTAGGCGCAGCTGTGAGAGAGTGTGTGTA 1419  
Db 1978 TG---CAGCTGCCACTGTTTTCAGGCGGCGACCGCGGCTGCTGCGGCACTGTCTCTGG 2034  
QY 1420 AGCTGACGCGCCAGACCTACTCAGAGTGAATATGTATGCGGCAAGAGACATGTGCC 1479  
Db 2035 CCCTGCGGCGCGCTTCTGCAAGCGGCGAGTACCTCATCCCAAGCGCATGCCCTGC 2094  
QY 1480 AAGAGATGTACATCCGAGAGGTCACTGGCGCTGTGGCAGATG 1527  
Db 2095 AGGCTCTACTTTTGTCTGTCTGCTCCATGGAGTGTCTCAAGGTG 2142

## RESULT 15

US-09-600-776-5  
; Sequence 5, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; CURRENT FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3064  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)...(3057)  
US-09-600-776-5

Query Match 2.2%; Score 49.8; DB 4; Length 3064;

Best Local Similarity 45.5%; Pred. No. 0.0016;

Matches 217; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 1049 CAGGGAAGAAGTACCTTTTCATGTTGGGCGACTTCTGCTGGCGCTCATGTTGGTTTCG 1108  
Db 1347 CACGACGCGGAGAAGATCTTCTCATCTGCACGATGCTCATAGGCGCTGTATGACGCG 1406  
QY 1109 CACCATCATGGTAGCATGAGCTCTGTCTATCTACACATGAACATGCAGATGCGGCTT 1168  
Db 1407 TGTGTGTCTGGGAACGTCAGGACCTCAAGGACTTTCATCGTGTGACCGCTGCGGCG 1466  
QY 1159 CTACCCAGATCATGCACTGTGTGAAGAAGTACATGAAGTGCAGCACGTCACCGAAGCT 1228  
Db 1467 CCACAGCGCATGAAGGACCTCAAGGACTTTCATCGTGTGACCGCTGCGGCGCGCT 1526  
QY 1229 GGAGCGGAGTATTGATGCTGGTATCAGCACTGCAGATCAACAAGAGATGACCAAGA 1288

Db	1527	CAAGCAGCGCATGCTCGAATACTTCCAGACCACGTTGGCCGCTCAACAGCGGCATCGAGC	1586
Qy	1289	GGTAGCCATCTTACAGCACTTGCCTGAGCGCTGGGGCAGAGTGGCTGTCTGTGCA	1348
Db	1587	CAACGAGTTACTGCGTGACTTCCAGACGAGCTGAGAGCTGACATTTGCTATGCACTGAA	1646
Qy	1349	CCTGTCCACTCTGAGCCGGGTGCAGATCTTTCAAGAACTGTGAGGCCAGCCTGCTGGAGGA	1408
Db	1647	TCGGGAGATCCTGCAGCTGCCGTTGTTTCGGGGCAGCGAGCAGGGGCTGCCTGCCGGCC--	1704
Qy	1409	GCTGGTGTGAAGTGCAGCCCCCAGACCTACTACAGGTGAATATGTATGCCGCAAGG	1468
Db	1705	-CTATCGCTGCACATCAAGACCTCGTTCTGCGCTCCGGCCGAGTACCTGTTCGCCCGTGG	1763
Qy	1469	AGACATTGGCCCAAGAGATGTATCATCATCCGAGAGGTTCAACTGGCCCGTGGTGGCAGA	1525
Db	1764	GGATGCCCTGCGGCACATTACTATGTCTCGGCTCGCTTGAGGTGCTCCGAGA	1820

Search completed: September 10, 2004, 20:28:53  
 Job time : 169.122 secs

Blank sheet

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	78.4	4.5	1307	4	US-09-172-422-3	Sequence 3, Appli
2	70.2	4.1	1507	4	US-08-997-685A-5	Sequence 5, Appli
3	65.8	3.8	1790	4	US-08-997-685A-11	Sequence 11, Appli
4	59.8	3.5	3480	3	US-09-226-012-1	Sequence 1, Appli
5	59.8	3.5	3950	3	US-09-226-012-3	Sequence 3, Appli
6	56	3.2	1584	4	US-08-997-685A-3	Sequence 3, Appli
7	53.6	3.1	3249	4	US-09-358-383C-3	Sequence 3, Appli
8	53.6	3.1	3355	4	US-09-358-383C-1	Sequence 1, Appli
9	52.8	3.1	7218	1	US-08-232-463-14	Sequence 14, Appli
c	52.4	3.0	7218	1	US-08-232-463-14	Sequence 14, Appli
10	52	3.0	3249	4	US-09-343-494-2	Sequence 2, Appli
11	52	3.0	3323	4	US-09-600-776-1	Sequence 1, Appli
12	52	3.0	3323	4	US-09-600-776-1	Sequence 1, Appli
13	50.8	2.9	3041	4	US-09-694-777A-19	Sequence 19, Appli
14	50.4	2.9	3857	4	US-09-336-643A-19	Sequence 19, Appli
15	49.8	2.9	3064	4	US-09-600-776-5	Sequence 5, Appli
16	49	2.8	3141	2	US-08-956-242-1	Sequence 1, Appli
17	49	2.8	3141	3	US-09-351-215-1	Sequence 1, Appli
18	45	2.6	505	4	US-09-621-976-15639	Sequence 15639, A
19	44	2.5	4722	4	US-08-979-608A-14	Sequence 14, Appli
20	44	2.5	4722	4	US-09-517-849-14	Sequence 14, Appli
21	44	2.5	4722	4	US-09-616-289-14	Sequence 14, Appli
22	42.8	2.5	2886	4	US-09-694-777A-13	Sequence 13, Appli
23	42.8	2.5	2967	4	US-09-694-777A-14	Sequence 14, Appli
24	42.8	2.5	3002	4	US-09-694-777A-1	Sequence 1, Appli
25	42.8	2.5	3083	4	US-09-694-777A-2	Sequence 2, Appli
26	41.8	2.4	364	4	US-09-621-976-17202	Sequence 17202, A
27	41.8	2.4	809	2	US-08-370-909-1	Sequence 1, Appli









Db 1673 TGACAGAGCCTCCTGACGAGCTGGCGCAGACATCGCCATGCACTGTCACAAGAGGTCC 1732  
QY 1028 TGACCCGGGTGACAGATCTTTGAGAACTGTGAGCCAGCCTCTGGAGAGCTGGTGTGA 1087  
Db 1733 TG---CAGCTCCCGCTGTTGAGGAGCAGCCGCGGCTGCTCGGGCACTGCTCTGG 1789  
QY 1088 AGCTGACGCCCCAGACCTTACTCACAGGTGAATATGTATGCGCAAGAGACATTTGCC 1147  
Db 1790 CCCTGGCGCCGCTTCTGACGCGCGGCGAGTACCTCATCCACAGGCGATGCCCTGC 1849  
QY 1148 AAGAGATGTACATCATCGAGAGGTTCACTGGCCGTTGGTGGCAGATG 1195  
Db 1850 AGGCCCTCTACTTTGCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTG 1897

## RESULT 8

US-09-358-383C-1  
; Sequence 1, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A. J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358.383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3355  
; TYPE: DNA  
; ORGANISM: Macaca sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (104)..(3352)  
US-09-358-383C-1

Query Match 3.1%; Score 53.6; DB 4; Length 3355;  
Best Local Similarity 45.6%; Pred. No. 8.8e-05;  
Matches 268; Conservative 0; Mismatches 314; Indels 6; Gaps 2;  
QY 611 CGGACCCCGCGCAGCCTGGCTTTGAGCGCCTGCGCGCCAGTACTCTATAGCTTTTACT 670  
Db 1416 CGGGCTGGAGCTGAGCGGCCGCTGCTGCGCAGGCTATACCTCCCTCTACT 1475  
QY 671 TCTCCAGCTGATACTGACTACATGGG---CGATACCGCCGCCAGCCAGGAAGAAG 727  
Db 1476 TCGCACTCAGCAGCCTCACCAGCGTGGGCTTCGGCAACGTTCGGCCAAACACGACACTG 1535  
QY 728 AGTACCTCTTCATGGTGGGACTTCTGCTGGCGGTCATGGTTTCGCCACCATCATGG 787  
Db 1536 AGAAGATCTTCTCCATCTGACCATGCTCATCGCGCCCTGATCGACGCGGTGTTGTCG 1595  
QY 788 GTAGCATGAGTCTGTCTATCTACAACTGAACACTGCGAGATGCGGCTTTTACCCAGATC 847  
Db 1596 GGAACGTGACGCCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACCAACAGCGCA 1655  
QY 848 ATGACTGGTGAAGAAGTACATGAAGTGTGACAGCTGAACCCGCAAGCTGGAGCGCGAG 907  
Db 1656 CGCGCAGCTGCGGACTACATCCGCTATCCACCGTATCCCAAGCCCTCAAGCAGCGCA 1715  
QY 908 TTATTGACTGTATCAGCACTGAGATCAACAGAGATGACCAACGAGTAGCCATCT 967  
Db 1716 TGCTGGAGTACTTCAGGCCACCTGGCGGTGGAACAATGGCATCGACCAACCGAGCTGC 1775  
QY 968 TACAGCACTTGCCTGAGCGGCTGGCGCAGAAAGTGGTGTGCTGTGCACTGTGCCACTC 1027  
Db 1776 TGCAGACCTCCCTGACGAGCTGGCGCAGACATCGCCATGACCTGCAACAGAGGTCC 1835  
QY 1028 TGACCCGGGTGACAGATCTTTGAGAACTGTGAGGCCAGCCTGCTGGAGAGCTGTGCTGA 1087  
Db 1836 TG---CAGCTGCCGCTGTTTGGAGCAGCAGCCGCGGCTGCTGCGGGCACTGTCTCTGG 1892

QY 1088 AGCTGACGCCCCAGACCTTACTCACAGGTGAATATGTATGTCGCAAGAGACATTTGCC 1147  
Db 1893 CCCTGGCGCCGCTTCTGACGCGCGGCGAGTACCTCATCCACAGGCGATGCCCTGC 1952  
QY 1148 AAGAGATGTACATCATCGAGAGGTTCACTGGCCGTTGGTGGCAGATG 1195  
Db 1953 AGGCCCTCTACTTTGCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTG 2000

## RESULT 9

US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 3.1%; Score 52.8; DB 1; Length 7218;  
Best Local Similarity 2.4%; Pred. No. 0.00021;  
Matches 9; Conservative 223; Mismatches 150; Indels 0; Gaps 0;  
QY 1340 AGGAGACCTTCGGGAGGTGCTGAGCGAGTATCCACAAGCACACATCATCGAGGAGA 1399  
Db 1436 ACRR 1377  
QY 1400 AAGACGTGAGATCTGCTGAAATGAACAAGTTGACGTGAATGCTGAGGAGCTGAGA 1459  
Db 1376 RRR 1317  
QY 1460 TCGCCTGACGAGGCGCACAGAGTCCCGGCTACGAGCCCTAGACCAGCAGCTGATGATC 1519



Db 1493 GGAACGTGACGGCCATCATCAGCGCATGTAGCGCCCGCGCTTTCTGTACACAGCGCA 1552  
QY 848 ATGCACTGGTGAAGAGTACATGAGCTGAGCAGCTCAACCGCAAGCTGAGCGCGAG 907  
Db 1553 CGCGGACCTGGGAGTACATCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCA 1612  
QY 908 TTATTGACTGGTATCAGCACCTGCAGATCAACAAGAGATGACCAACGAGGTAGCATCT 967  
Db 1613 TGCTGGAGTACTTCAGGCGCACTGGCGGGTGAACAATGGGATCGACACCGAGTGCC 1672  
QY 968 TACAGCACTTCCTGAGCGGCTGGGGCAGAGTGGCTGTGTCTGTGCACTGTCCACTC 1027  
Db 1673 TGCAGAGCTCCCTGACAGCTGGCGCAGACATCGCCATGCACCTGCAACGAGGTCC 1732  
QY 1028 TGAGCGGGTGCAGATCTTTAGAACTGTGAGGCGAGCTGTGAGGAGTGTGTGCTGA 1087  
Db 1733 TG--CAGCTGCCACTGTTTGGAGCGGCCAGCGCGGCTGTCTGGGCACTGTCTCTGG 1789  
QY 1088 AGCTGCAGCCCCAGACCTTACTCACCAGGTGAATATGTATGCGCAAGAGACATTTGCC 1147  
Db 1790 CCCTGGCGCCCGCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGCGATGCCCTGC 1849  
QY 1148 AAGAGATGTACATCATCGAGGGTCAACTGGCGTGTGGCAGATG 1195  
Db 1850 AGGCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTG 1897

## RESULT 12

US-09-600-776-1  
; Sequence 1, Application US/09600776  
; Patent No. 6326168

GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

FILE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT

CURRENT APPLICATION NUMBER: US/09/600,776  
; PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21  
; PRIOR FILING DATE: 1998-01-23

PRIOR FILING DATE: 1998-01-23  
; PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1

LENGTH: 3323  
; TYPE: DNA

ORGANISM: Homo sapiens  
; NAME/KEY: CDS

LOCATION: (6)...(3257)  
US-09-600-776-1

Query Match 3.0%; Score 52; DB 4; Length 3323;  
Best Local Similarity 45.4%; Pred. No. 0.00024;

Matches 267; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 611 CGGACCGCGGCGGCTGGCTTTGAGCGCTGGCGGCGGAGTACTCTATAGCTTTTACT 670

Db 1318 CGGGCTGGAGCTGCTGGGCGGCGGCTGGCTGGCGGCGGCTATACCTCCCTCTACT 1377

QY 671 TCTCCAGCTGATATGACTACAGTGGG--CGATACACGCGCGCCAGCGGGAAGAG 727

Db 1378 TCGCACTCAGAGCTCACCAGCTGGCTTGGCAAGGTGTCGCGCAACACGACACCG 1437

QY 728 AGTACCTTTTCANGGTGGGAGCTTCCTGTGGCGGCTCATGGTTTGGCCACCATCATGG 787

Db 1438 AGAAGATCTTCTCCATCTGCACCATGCTCATCGCGGCGGCTGATGACGCGGTGGTGTG 1497

QY 788 GTAGCATGAGCTGTGTCTATACAACTGAACATGTGAGATGCGGCTTTCTACCCAGATC 847

Db 1498 GGAACGTGACGGCCATCATCGCGGCTATGACGCGCGGCTTTCTGTACACAGCGCA 1557

QY 848 ATGCACTGGTGAAGAGTACATGAGCTGAGCAGCTCAACCGCAAGCTGGAGCGGAG 907  
Db 1558 CGCGGACCTGGGAGTACATCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCA 1617  
QY 908 TTATTGACTGGTATCAGCACCTGCAGATCAACAAGAGATGACCAACGAGGTAGCATCT 967  
Db 1618 TGCTGGAGTACTTCAGGCGCACTGGCGGGTGAACAATGGGATCGACACCGAGTGCC 1677  
QY 968 TACAGCACTTCCTGAGCGGCTGGGGCAGAGTGGCTGTGTGTGCACTGTCCACTC 1027  
Db 1678 TGCAGAGCTCCCTGACAGCTGGCGCAGACATCGCCATGCACCTGCAACGAGGTCC 1737  
QY 1028 TGAGCGGGTGCAGATCTTTAGAACTGTGAGGCGAGCTGTGAGGAGTGTGTGCTGA 1087  
Db 1738 TG--CAGCTGCCACTGTTTGGAGCGGCCAGCGCGGCTGTCTGGGCACTGTCTCTGG 1794  
QY 1088 AGCTGCAGCCCCAGACCTTACTCACCAGGTGAATATGTATGCGCAAGAGACATTTGCC 1147  
Db 1795 CCCTGGCGCCCGCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGCGATGCCCTGC 1854  
QY 1148 AAGAGATGTACATCATCGAGGGTCAACTGGCGTGTGGCAGATG 1195  
Db 1855 AGGCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTG 1902

## RESULT 13

US-09-694-777A-19

; Sequence 19, Application US/09694777A

; Patent No. 6638736

GENERAL INFORMATION:

; APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL

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; APPLICANT: BECKH, SYNNOVE

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; APPLICANT: PEREZ, ARACELI SANCHEZ

; APPLICANT: WESELOH, RUDIGER

TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS

TITLE OF INVENTION: THEREOF

FILE REFERENCE: MFG-8

CURRENT APPLICATION NUMBER: US/09/694,777A

CURRENT FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: PCT/EP99/02695

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EP 98 10 7268.9

PRIOR FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 3041

TYPE: DNA

ORGANISM: Bovine sp.

US-09-694-777A-19

Query Match 2.9%; Score 50.8; DB 4; Length 3041;

Best Local Similarity 44.5%; Pred. No. 0.0005;

Matches 245; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

QY 652 TACCTCTATAGCTTTTACTTCTCCACGCTGATCTACTACTAGTGGGC---GATACACCG 708

Db 1305 TACATCTCTCGTTGTATTTTCCATGACGAGCTCACCAGCGTGGGCTTTGGAAATC 1364

QY 709 CGGCACCGAGGAAGAGTACCTTTCATGGTGGGCGACTTCTGTGGCGGCTCATG 769

Db 1365 GCCCGCTCCACAGACATTGAGAAGATCTTTGCCGTGGCCCATGATGATTTGGCTCCTC 1424

QY 769 GGTTCGCCACCATCATGGGTAGCATGAGCTTGTCTATCTACACATGACACTGACAT 828

Db 1425 CTCTATGCCACCATCTTTTGGGAATGTGACACCATTTTCCACAGATGTACGCCAAC 1484

QY 829 CGCGCTTTCTACCCAGATCATGCACTGGTGAAGAGTACATGAAGCTGACGAGCTCAAC 888

Db 1485 AACAGGTACCATGAGATGCTCAACAGTGTCCGGGACTTCTTGAAGCTTCTACAGGTGCC 1544



Db 1527 CAAGCAGCGCATGCTCGAATACTTCCAGACCACGCTGGGCCGTCAACAGCGGCATCGACGC 1586  
QY 957 GGTAGCCATCTTACAGCACTTGCCTGAGCGGCTGCGGGCAGAGTGGCTGTGTCTGTGCA 1016  
Db 1587 CAACGAGTTACTGCGTGACTTCCAGACGAGCTGAGAGCTGACATTGCTATGCACCTGAA 1646  
QY 1017 CCTGTCCACTCTGAGCCGGGTGCAGATCTTTTCAGAACTGTGAGGCCAGCCTGCTGGAGGA 1076  
Db 1647 TCGGAGATCCTGCAGCTGCCGTTGTTGCGGGCAGCGAGCGGGGCTGCCCTGCGGGCC-- 1704  
QY 1077 GCTGGTCTGAAGCTGCAGCCCCCAGACCTACTACCAAGTGAATATGTATGCCCCGAAAGG 1136  
Db 1705 -CTATCGCTGCACATCAAGACCTCGTTCTGGCTCCGGCGAGTACCTGTTGGCCCGTGG 1763  
QY 1137 AGACATTGGCCCAAGAGATGTACATCCGAGAGGTCAACTGCCCGTGGTGGCAGA 1193  
Db 1764 GGATGCCCTGCAGGCACATTACTATGTCTGCTCCGGCTCGCTTGAGGTGCTCCGAGA 1820

Search completed: September 10, 2004, 20:28:58  
Job time : 127.878 secs

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